

10/001,245



# FIG. 1

Bet v 1 sense	5' - AATTATGAGACTGAGACCA <u>CCTCTGTTATCCCAGCAGCTCG</u> -3'
Bet v 1 non-sense	3' - TTAATACTCTGACTCTGG <u>GGAGACAATAGGGTCGTCGAGC</u> -5'
sense primer	5' - <u>TGAGACCC</u> CTCTGTTATCCCAG -3'
non-sense primer	3' - ATACTCTGACTCTGG <u>GGAGACA</u> -5'

10/001,245



## FIG. 2

all	sense	1: 183Bv, 15-mer 5'-GTTGCCAACGATCAG
1	sense	2: 184Bv, 23-mer 5'-TGAGACCCCTCTGTTATCCAG
1	non-sense	3: 185Bv, 23-mer 5'-ACAGAGGGGGTCTCAGTCTCATA
2	sense	4: 186Bv, 31-mer 5'-GATACCCTCTTCCACAGGTTGCACCCCAAG
2	non-sense	5: 187Bv, 31-mer 5'-ACCTGTGGAAAGAGGGTATGCCATCAAGGA
3	sense	6: 188Bv, 23-mer 5'-AACATTCAGGAAATGGAGGGCC
3	non-sense	7: 189Bv, 23-mer 5'-TTCCCTGAAATGTTTCAACACT
4	sense	8: 190Bv, 23-mer 5'-TTAAGAACATCAGCTTCCGAA
4	non-sense	9: 191Bv, 23-mer 5'-AGCTGATGTTCTTAATGGTTCCA
5	sense	10: 192Bv, 23-mer 5'-GGACCATGCAAACCTCAAATACA
5	non-sense	11: 193Bv, 23-mer 5'-AGTTGCATGGTCCACCTCATCA
6	sense	12: 194Bv, 23-mer 5'-TTCCCTCAGGCCCTCCCTTCAA
6	non-sense	13: 195Bv, 23-mer 5'-AGGCCTGAGGGAAAGCTGATCTT
7	sense	14: 196Bv, 24-mer 5'-TGAAGGATCTGGAGGGCTGGAAC
7	non-sense	15: 197Bv, 24-mer 5'-CCCTCCAGATCCTTCAATGTTTC
8	sense	16: 198Bv, 24-mer 5'-GGCAACTGGTGTGGAGGGATCCAT
8	non-sense	17: 199Bv, 24-mer 5'-CCATCACCACTGGCCACTATCTTT
all	non-sense	18: 200Bv, 15-mer 5'-CATGCCATCCGTAAG

10/001,245



## FIG. 3

## 1 (A-C)

GGTGTGTTAATTATGAGACTGAGACCACCTCTGTTATCCCAGCAGCTCGACTGTTCAAG 60  
 G V F N Y E T E T T - P S V I P A A R L F K 20

## 9 (A-G) 2 (A-C) 2 (A-C)

GCCTTTATCCTTGATGGCGATAACCTCTTCCAAGGTTGCACCCCAAGCCATTAGCAGT 120  
 A F I L D - G G D N - T L F P K - Q V A P Q A I S S 40

## 3 (GA-TC)

## 7 (AA-TC)

## 4 (G-C)

## 6 (GA-TC)

GTTGAAAACATTGAAGGAAATGGAGGGCCTGGAACCATTAAAGAAGATCAGCTTCCCGAA 180  
 V E N I E - S G N - S G G P G T I K K - N I S F P E - S 60

## 5 (CA-TG)

GGCCTCCCTTCAGTACGTGAAGGACAGAGTTGATGAGGTGGACCACACAAACTTCAAA 240  
 G L P F K Y V K D R V D E V D H T - A N F K 80

TACAATTACAGCGTGATCGAGGGCGGTCCCATAGCGACACATTGGAGAAGATCTCCAAC 300  
 Y N Y S V I E G G P I G D T L E K I S N 100

## 10 (GAG-CAC) 8 (CCC-TGG)

GAGATAAAAGATAGTGGCAACCCCTGATGGAGGATCCATCTTGAAGAGATCAGCAACAAAGTAC 360  
 E I K I V A T P - G D G G S I L K I S N K Y 120

CACACCAAAGGTGACCATGAGGTGAAGGCAGAGCAGGTTAAGGCAAGTAAAGAAATGGC 420  
 H T K G D H E V K A E Q V K A S K E M G 140

GAGACACTTTGAGGGCCGTTGAGAGCTACCTCTGGCACACTCCGATGCCTACAACTAA 480  
 E T L L R A V E S Y L L A H S D A Y N stop 159



FIG. 4

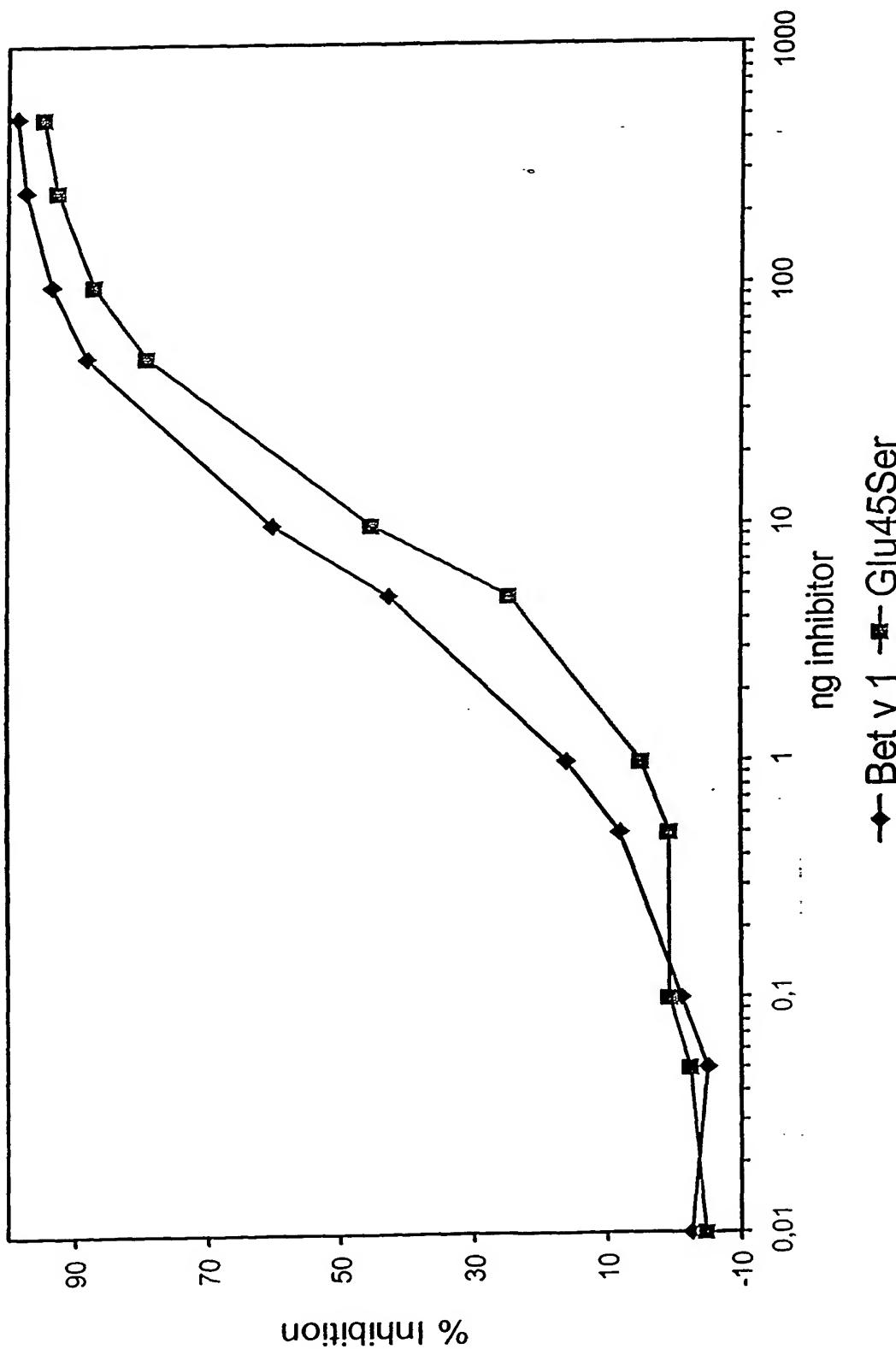
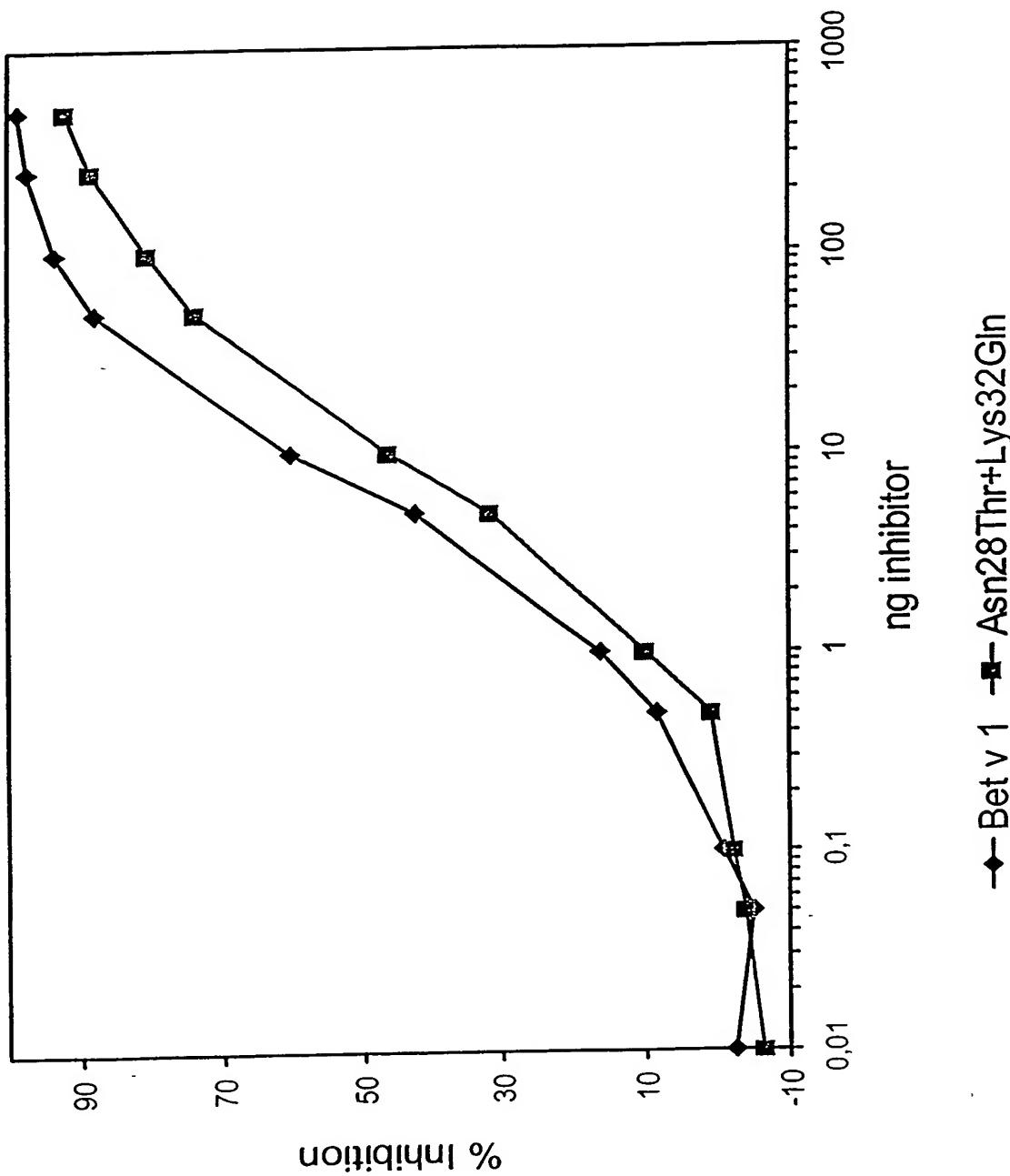




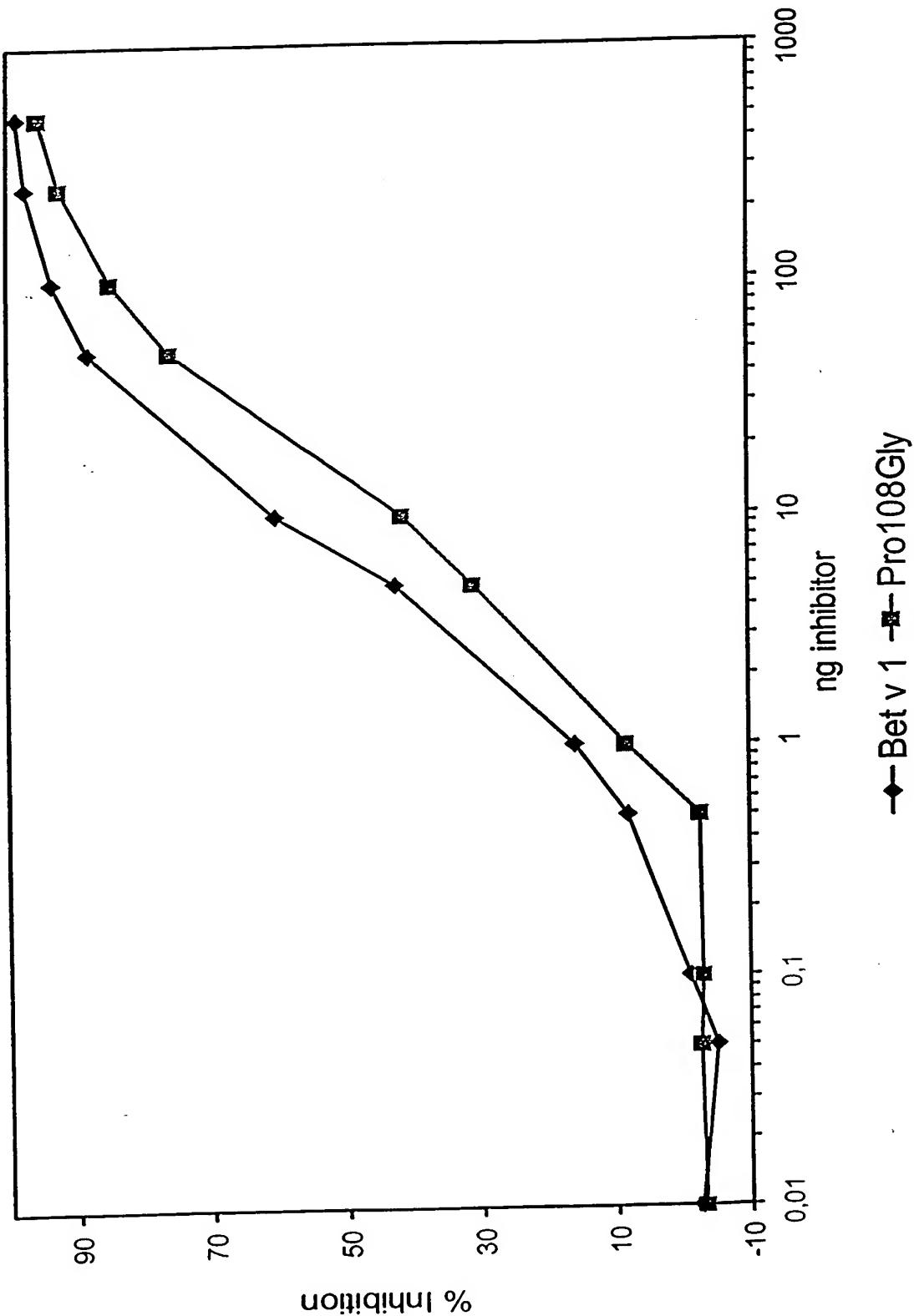
FIG. 5



10/001,245



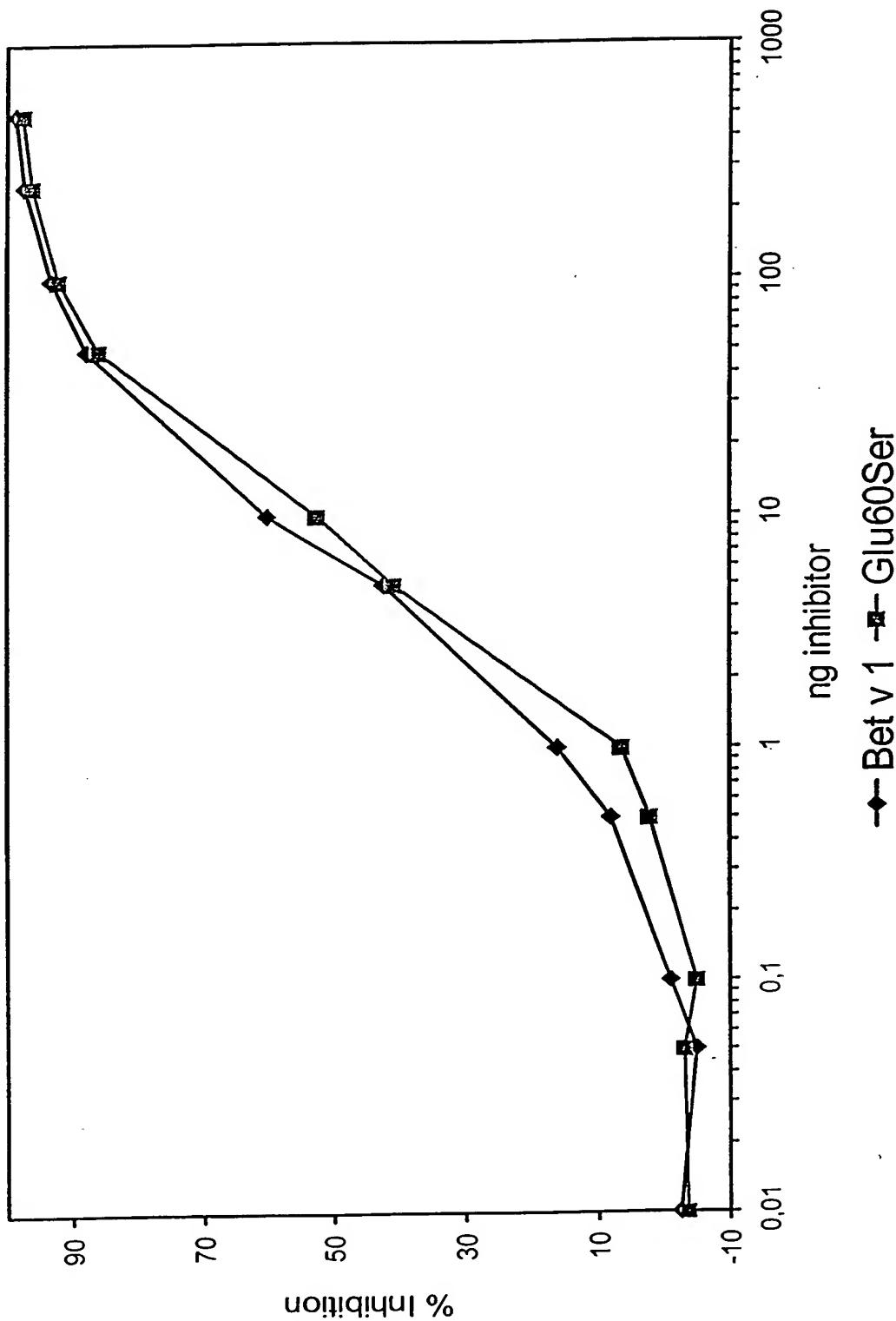
FIG. 6



10/001,245



FIG. 7



10/001,245



FIG. 8

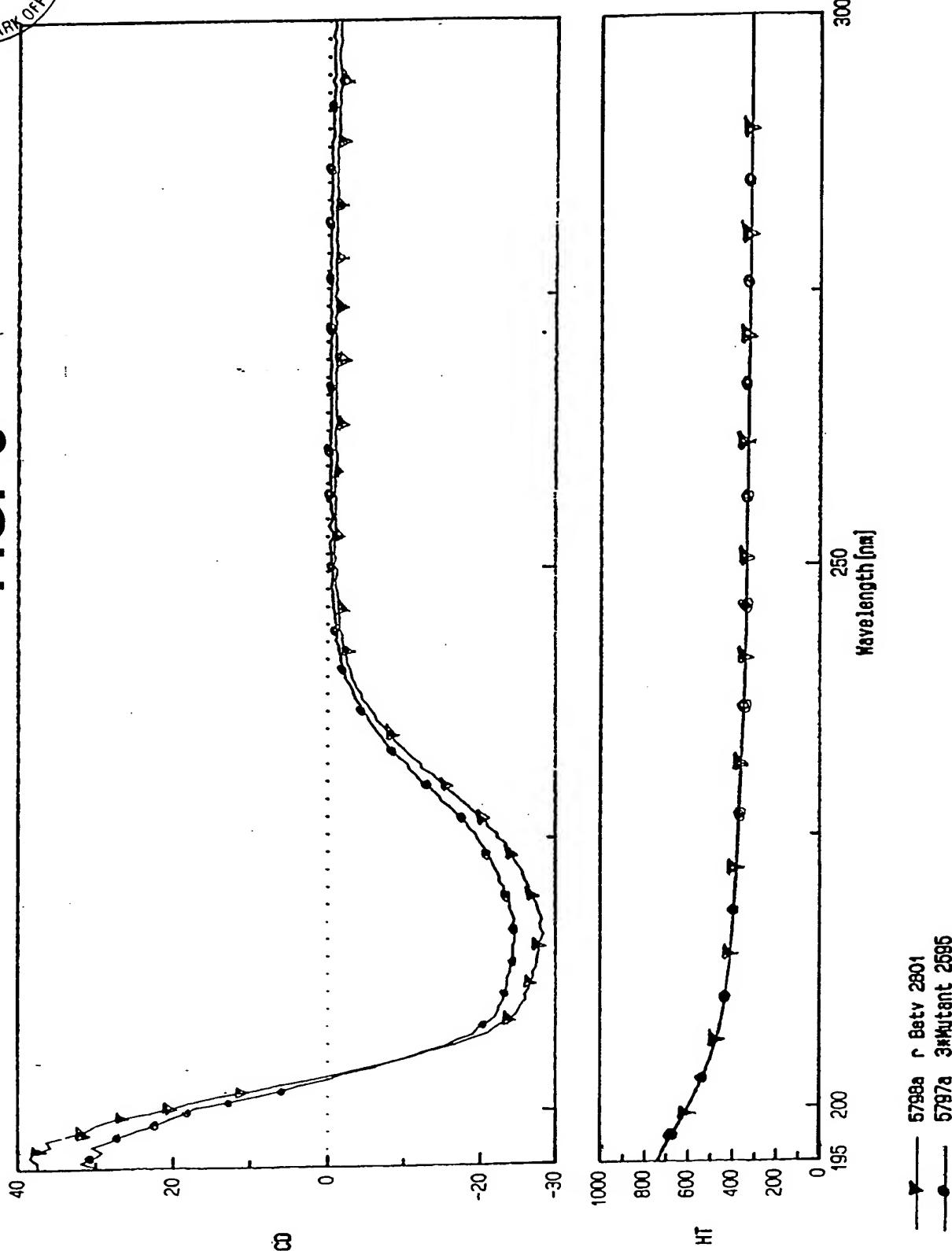
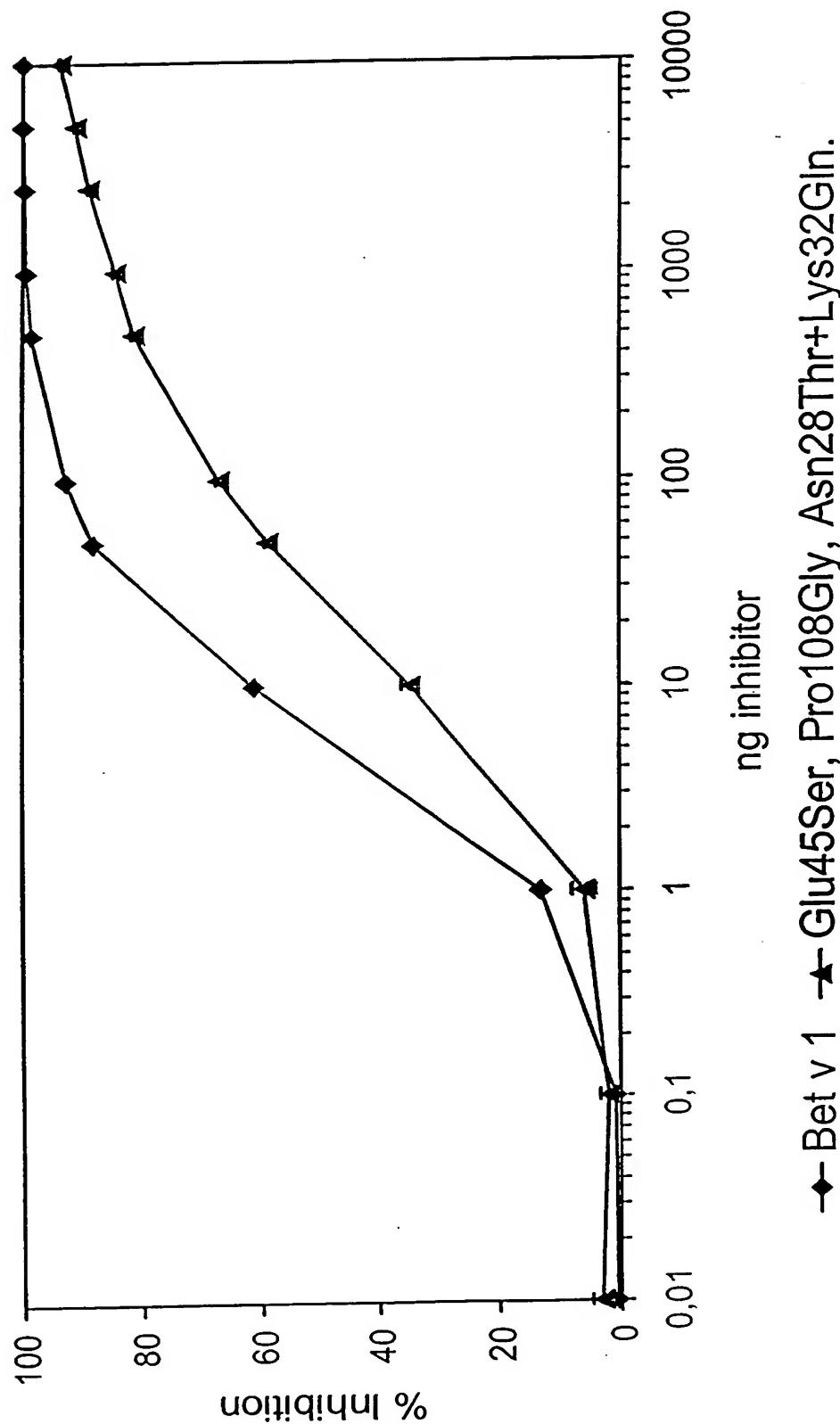


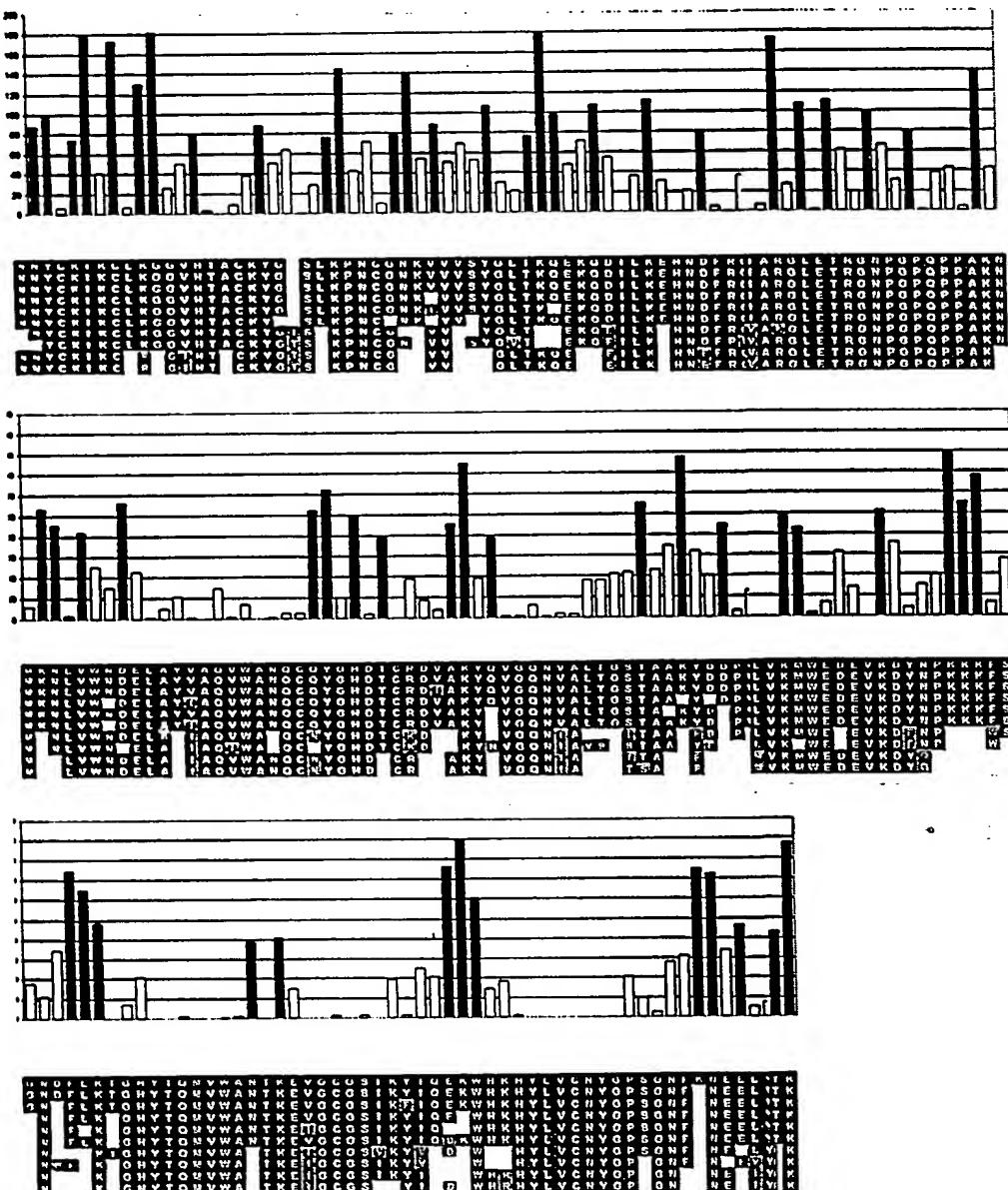
FIG. 9



10/001,245



## FIG. 10 A

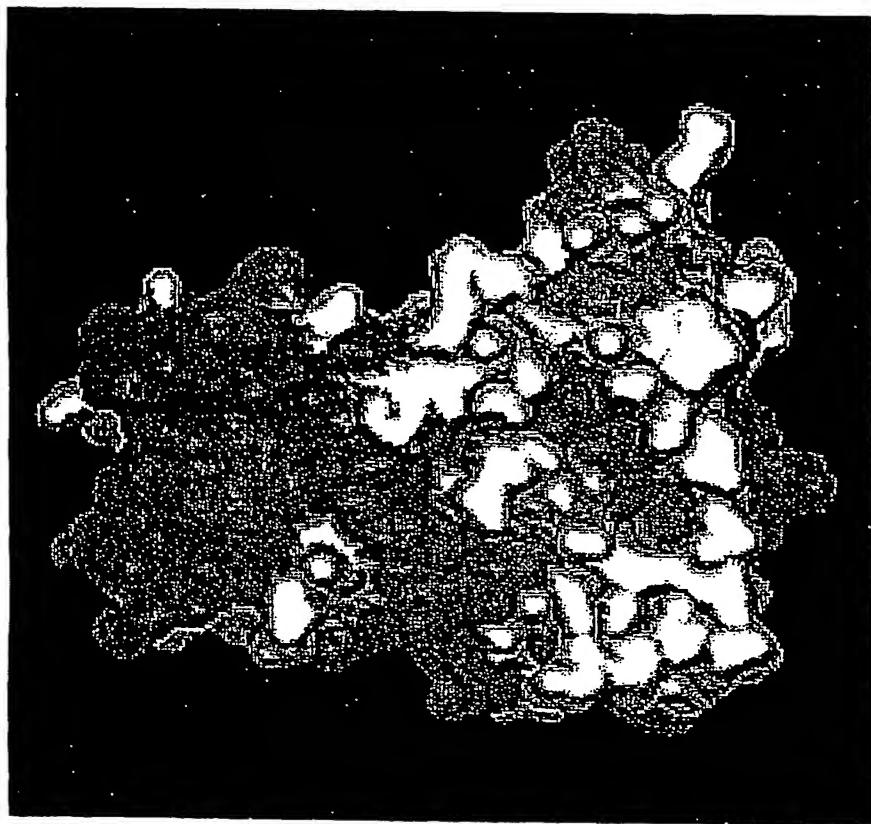


10001245 112602

10/001,245



## FIG. 10 B



10/001,245



## FIG. 11 A

### Ves v 5 mutant 1 (K72A)

Ves v 5 sense	5' - ACCACAGCCTCCAGCGAAGAATATGAAAAATTGGTATGGA	-3'
Ves v 5 non-sense	3' - TGGTGTCGGAGGTCGTTCTTATACTTTAAACCACACCT	-5'
sense primer	5' - CCAGCGG <u>CTAATATGAAAAAT</u>	-3'
non-sense primer	3' - GTCGGAGGTC <u>CGCCGATT</u> TATAC	-5'

## FIG. 11 B

### Ves v 5 mutant 2 (Y96A)

Ves v 5 sense	5' - GGCTAATCAATGTCATGGTCACGATACTTGCAGGGATG	-3'
Ves v 5 non-sense	3' - CCGATTAGTTACAGTTACCCAGTGCTATGAACGTCCCTAC	-5'
sense primer	5' - TGTCAAG <u>CTGGTCACGATACT</u>	-3'
non-sense primer	3' - TTAGTTACAG <u>TTCGACCAGTG</u>	-5'

## FIG. 12

all sense 1: XhoI start, 38-mer:

EcoRI  
 5' - CCGCTCGAGAAAAGAACAATTATTGTAAAATAAATG  
 L E K R N N Y C K I K  
 Kex2 cleavage site amino terminus of Ves v 5

1 sense	1: K72As	21-mer	5' - CCAGCGG <u>CTAATATGAAAAAT</u>
1 non-sense	2: K72Aa	21-mer	5' - CATATTAG <u>CCGCTGGAGGCTG</u>
2 sense	3: Y96As	21-mer	5' - TGTCAAG <u>CTGGTCACGATACT</u>
2 non-sense	4: Y96Aa	21-mer	5' - GTGACC <u>AGCTTGACATTGATT</u>
all non-sense	7: CT-pPICZ $\alpha$ A,	21-mer	5' - ATTCA <u>TAGCTGCGAGATA</u> GG

10/001,245



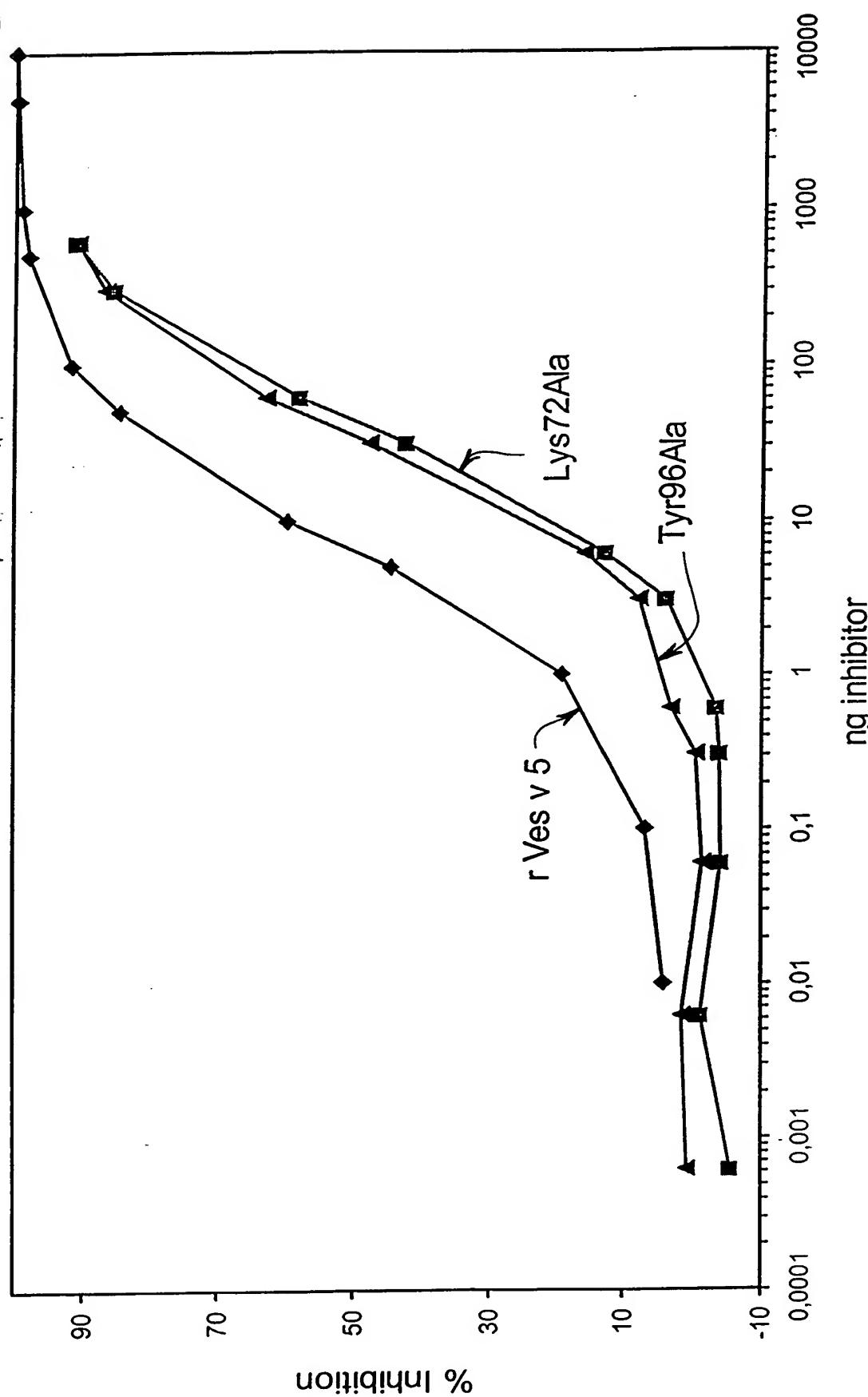
# FIG. 13

1	AACAATTATTGTAAAATAAAATGTTGAAAGGAGGTGTCCATACTGCCTGCAAATATGGA	60
1	N N Y C K I K C L K G G V H T A C K Y G	20
61	AGTCCTAACCGAATTGCGGTAAATAAGGTAGTGGTATCCTATGGTCTAACGAAACAAGAG	120
21	S L K P N C G N K V V V S Y G L T K Q E	40
121	AAACAAGACATCTTAAAGGAGCACAATGACTTAGACAAAAAATTGCACGAGGATTGGAG	180
41	K Q D I L K E H N D F R Q K I A R G L E	60
1 [K72A] (AAG-GCT)		
181	ACTAGAGGTAATCCTGGACCACAGCCTCCAGCG <u>AAGA</u> ATATGAAAAATTGGTATGGAAC	240
61	T R G N P G P Q P P A K N M K N L V W N	80
2 [Y96A] (TA-GC)		
241	GACGAGTTAGCTTATGTCGCCAAGTGTGGCTAATCAATGTCAAT <u>ATGGTCACGATA</u> CT	300
81	D E L A Y V A Q V W A N Q C Q Y G H D T	100
301	TGCAGGGATGTAGCAAAATATCAGGTTGGACAAAACGTAGCCTAACAGGTAGCACGGCT	360
101	C R D V A K Y Q V G Q N V A L T G S T A	120
361	GCTAAATACGATGATCCAGTTAAACTAGTTAAATGTGGGAAGATGAAGTGAAAGATTAT	420
121	A K Y D D P V K L V K M W E D E V K D Y	140
421	AATCCTAACGAAAAAGTTTGGGAAACGACTTTCTGAAAACGGCCATTACACTCAAATG	480
141	N P K K K F S G N D F L K T G H Y T Q M	160
481	GTTGGCTAACACCAAGGAAGTTGGTGTGGAAAGTATAAAATACATTCAAGAGAAATGG	540
161	V W A N T K E V G C G S I K Y I Q E K W	180
541	CACAAACATTACCTTGTATGTAATTATGGACCCAGCGGAAACTTTAAGAATGAGGAACCT	600
181	H K H Y L V C N Y G P S G N F K N E E L	200
601	TATCAAACAAAGTAA	612
201	Y Q T K stop	204

10/001,245

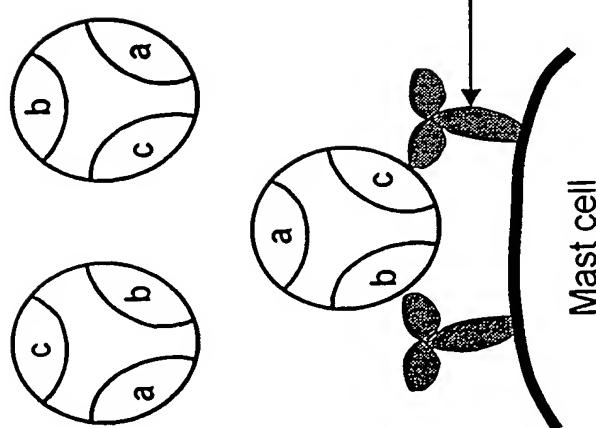


FIG. 14



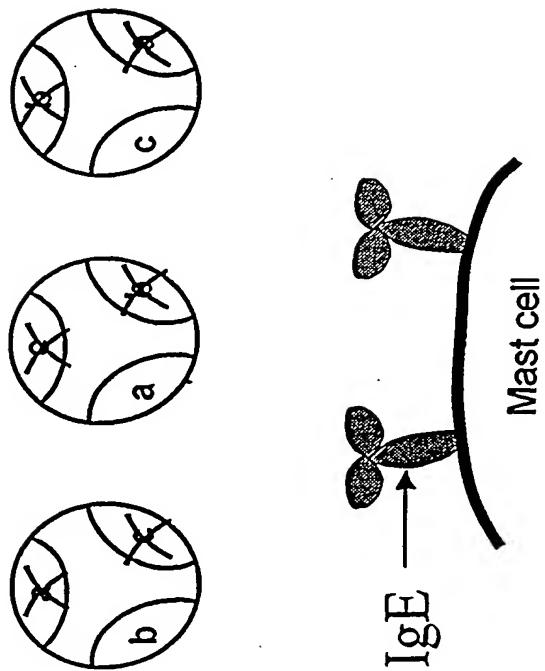


**FIG. 15 A**



Cross-linking

**FIG. 15 B**



No cross-linking

10/001,245



## FIG. 16 A

### DNA SEQUENCE

#### ORIGIN

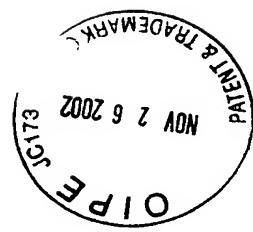
1        cacaattct tctttttcc ttactactga tcattaatct gaaaacaaaa ccaaacaaaac  
 61      cattcaaaat gatgtacaaa attttgtc tttcattgtt ggtcgccgagcc gttgctcgat  
 121     atcaagtcga tgtcaaagat tggccaaatc atgaaaatcaa aaaagtttg gtaccaggat  
 181     gccatggttc agaaccatgt atcattcatc gtggtaaacc attccaaatg gaagccgtt  
 241     tcgaagccaa ccaaaacaca aaaacggcta aaattgaaat caaagcctca atcgatggtt  
 301    tagaaggta tggtcccggt atcgatccaa atgcattgcca ttacatgaaa tgccattgg  
 361    ttaaaggaca acaatatgtat attaaatata catgaaatgt tccgaaaaatt gcaccaaaat  
 421    ctgaaaatgt tgtcgtaact gttaaagttt tgggtgatga tgggttttg gcctgtgcta  
 481    ttgctactca tgctaaaatc cgcgattaaa tcaaacaaaa ttatgtattt ttgtatcac  
 541    aatgatttga ttttttcc aaaaaaaaaaaa taaataaaat ttggaaattt c

## FIG. 16 B

1        mmykilclsi lvaavardqv dvkdcanhei kkvlvpgchq sepciihrgk pfqleavfea  
 61      nqntktakie ikasidglev dvpgidpnac hymkcpivkg qqydkytwv vpkiaapksen  
 121     vvvtkvmdg dgvlacaiat hakird

**FIG. 17**

10/001,245



10/001,245



## FIG. 18 A

DNA template: Bet v 1 (2589) carrying the Y5V mutation.

331pMalc (s)  
189BV (a)  
188BV (s)  
362BV (a)  
361BV (s)  
364BV (a)  
363BV (s)  
366BV (a)  
365BV (s)  
332pMalc (a)

## FIG. 18 B

DNA template: Bet v 1 (2571) carrying N28T, K32Q, P108G mutations.

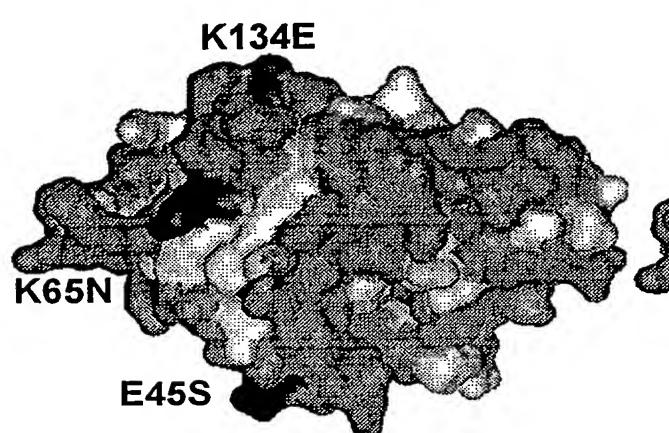
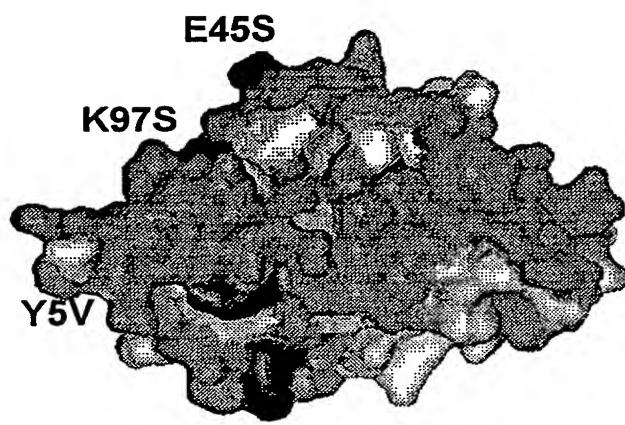
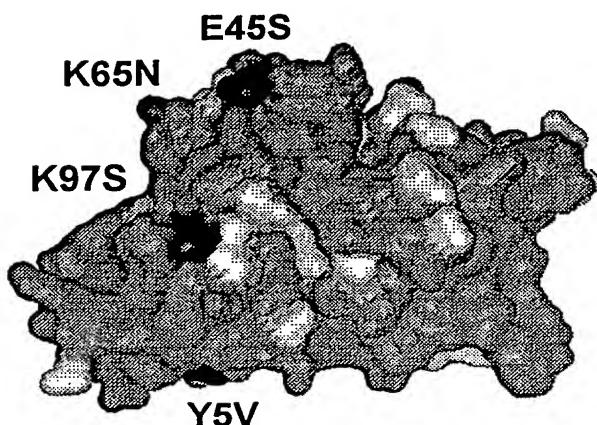
331pMalc  
368BVa  
367BVs  
370BVa  
369BVs  
372BVa

10/001,245



# FIG. 19 A

Bet v 1 (2628)

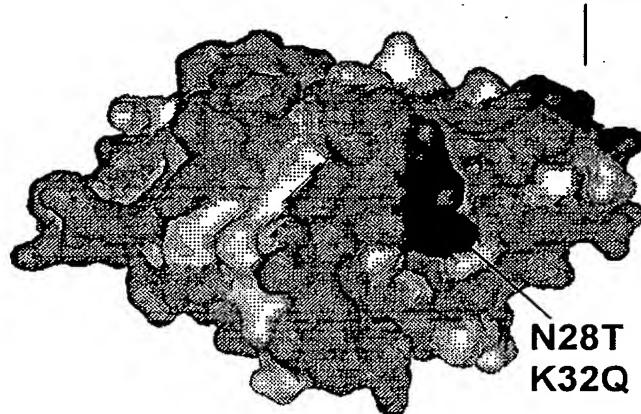
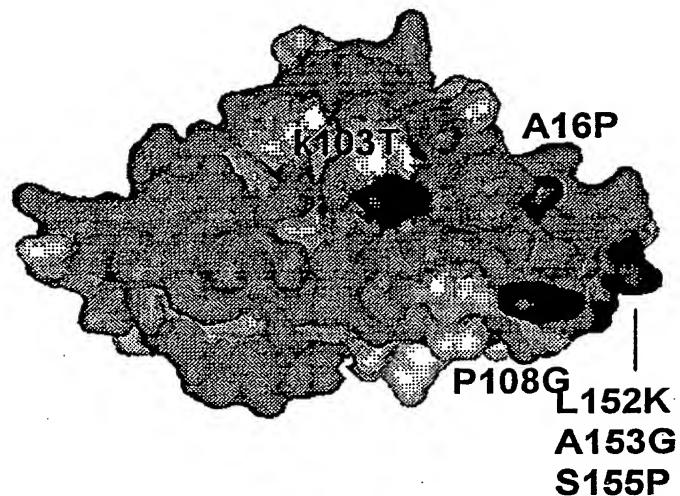
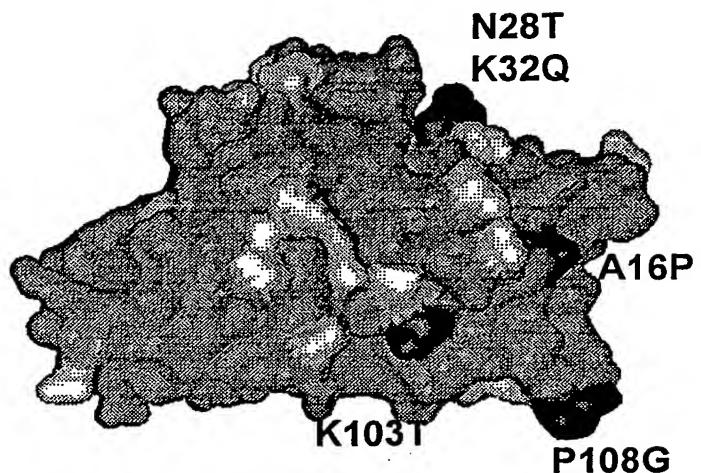


10/001,245



## FIG. 19 B

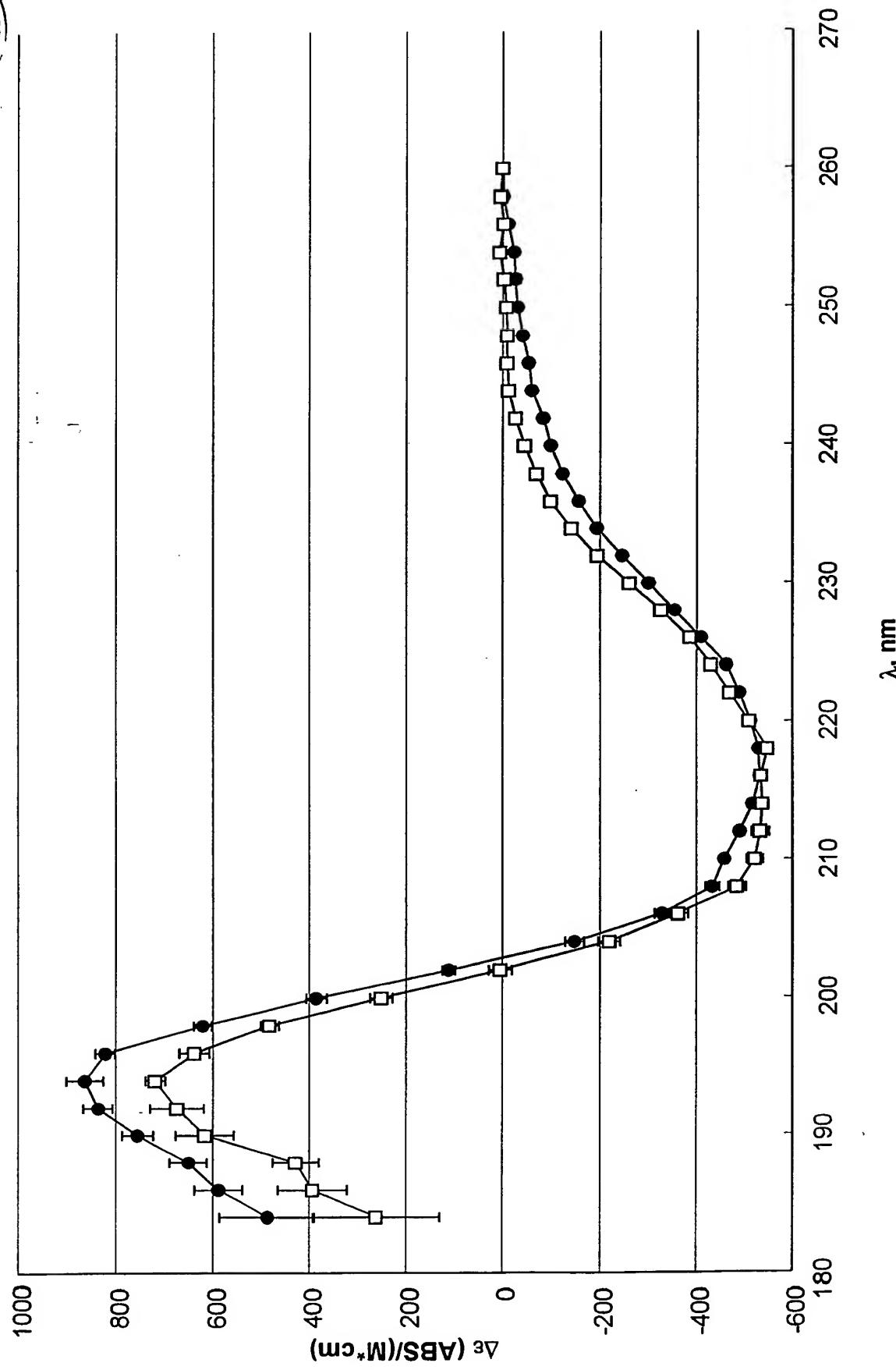
Bet v 1 (2637)



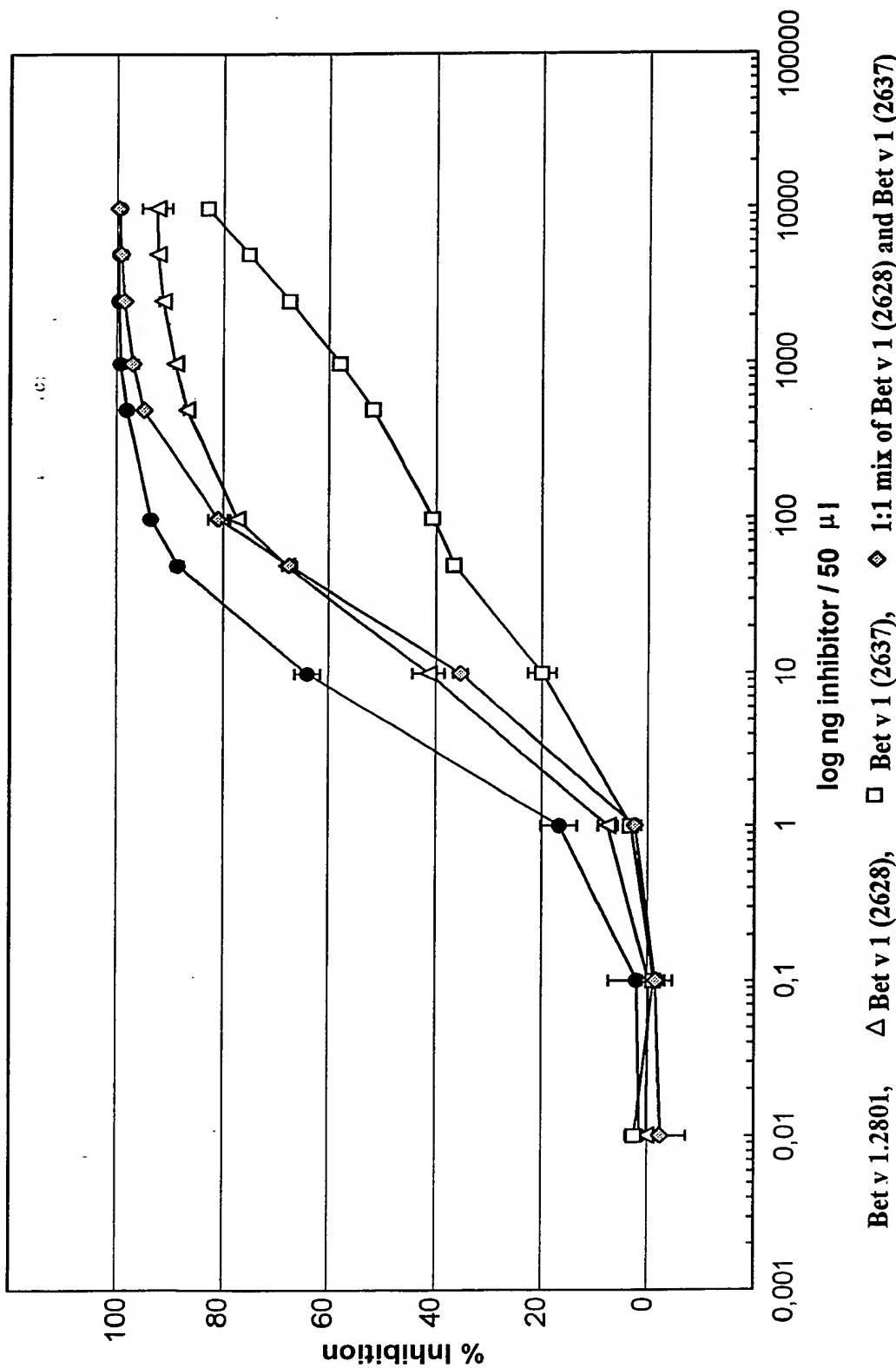
10/001,245



FIG. 20



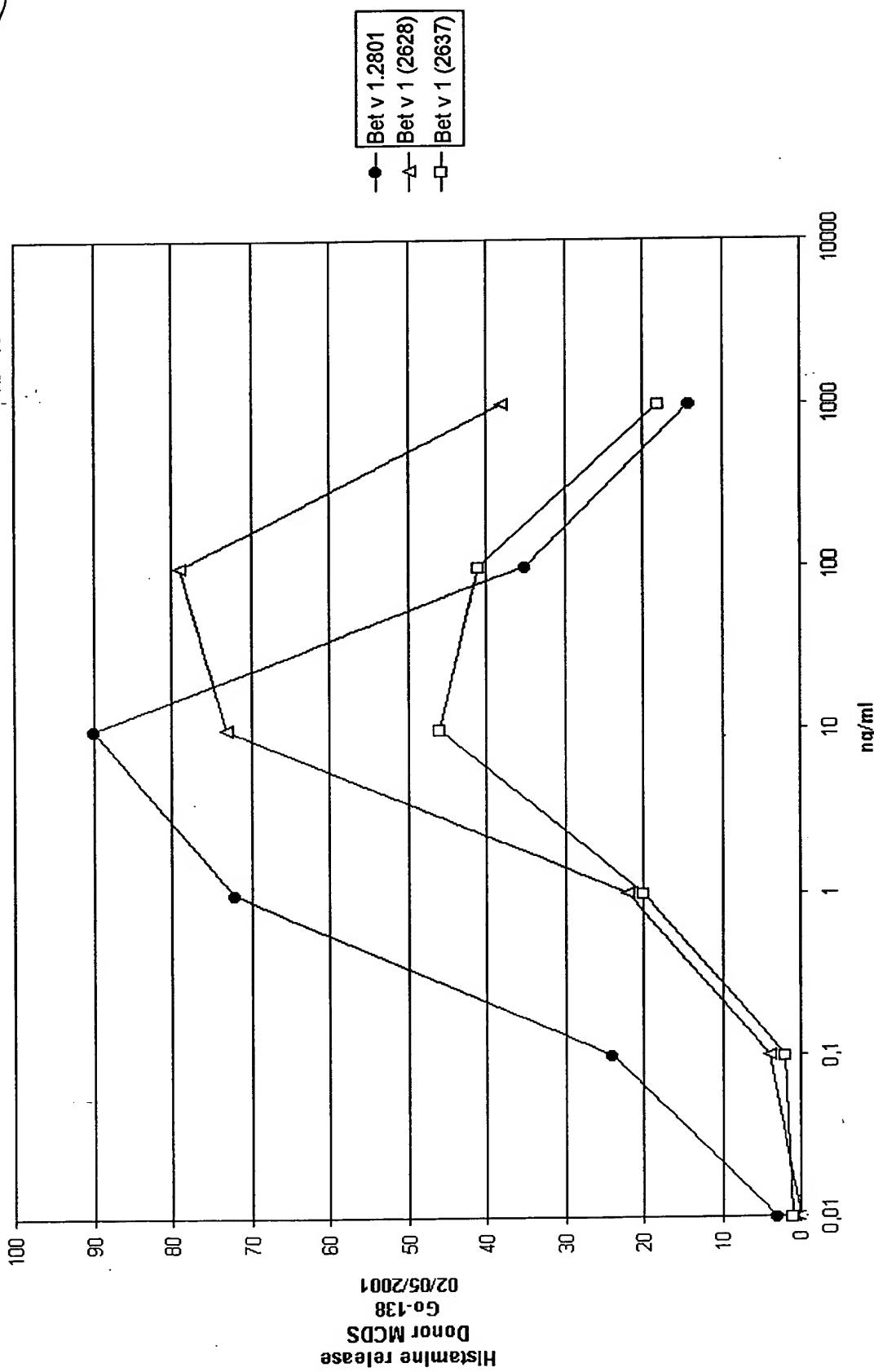
10/001,245

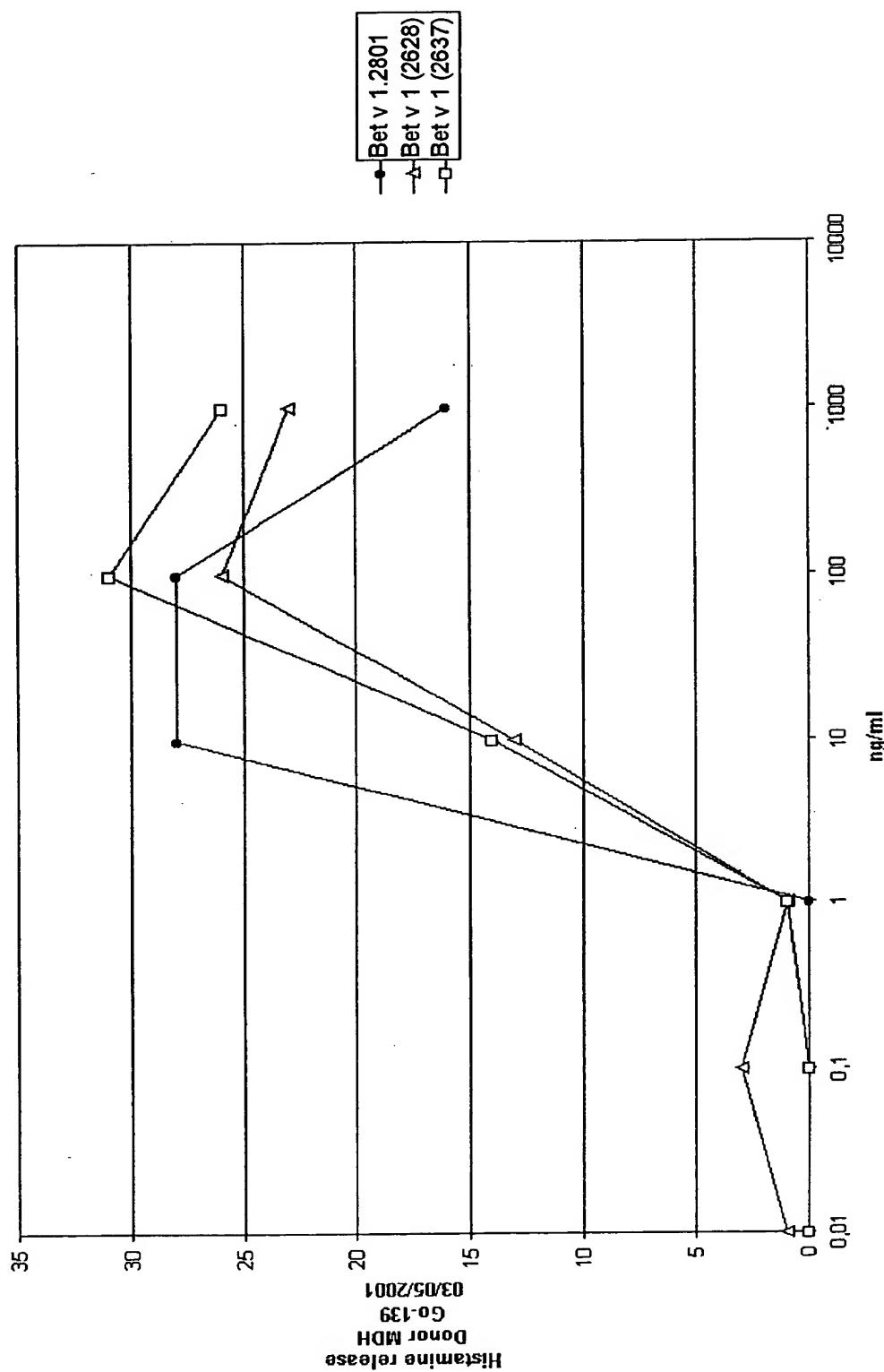
**FIG. 21**

10/001,245



FIG. 22

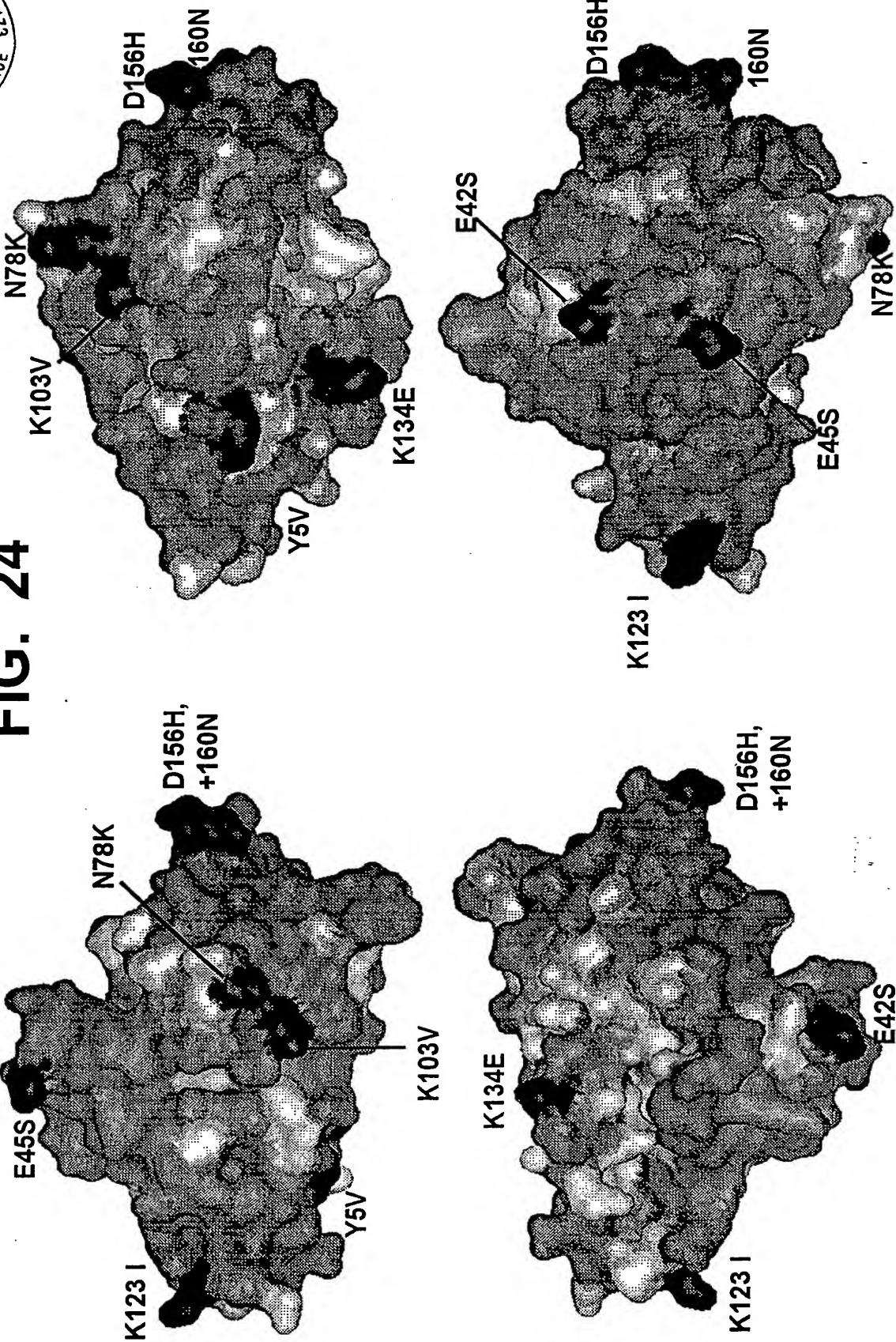


**FIG. 23**

10/001,245



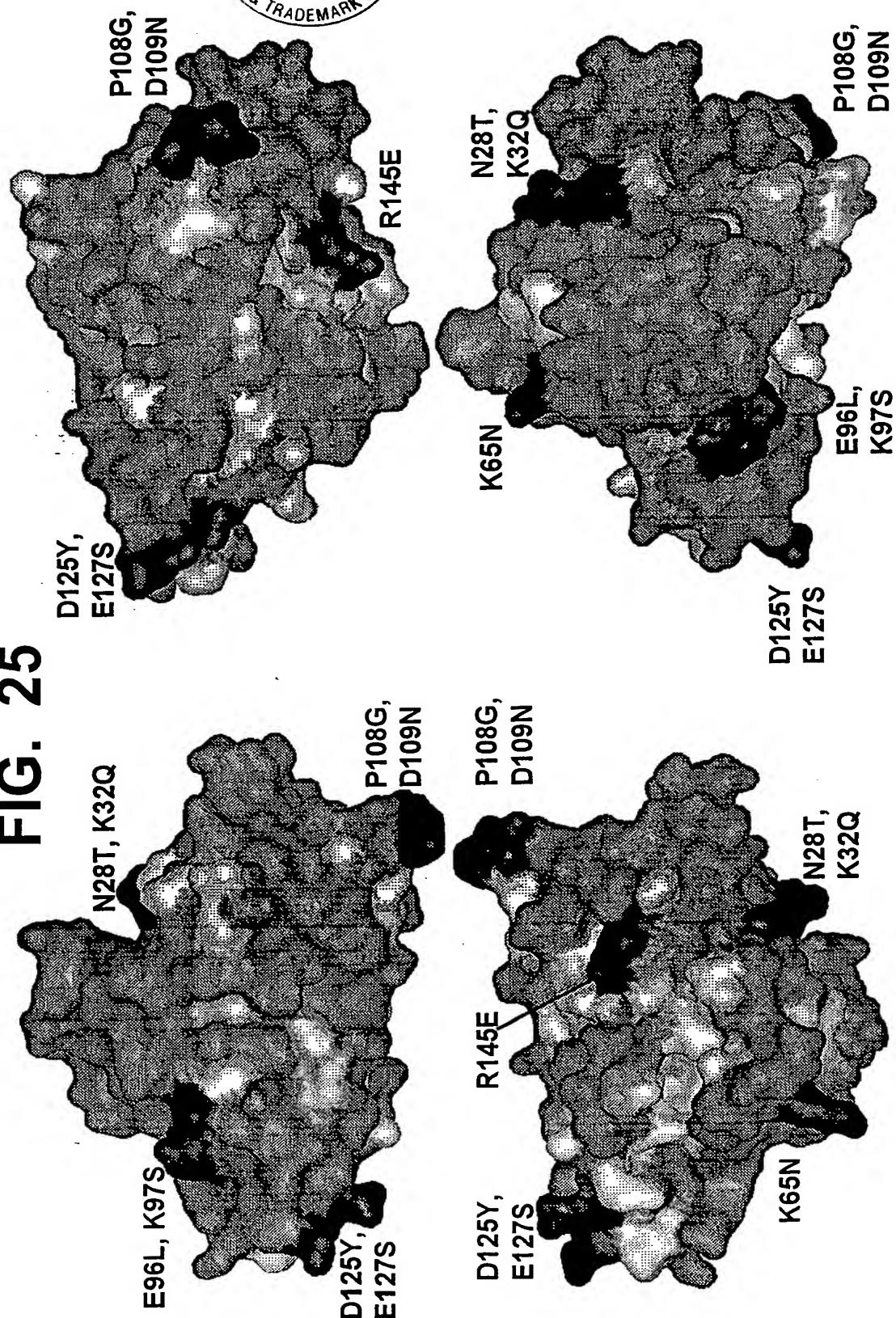
FIG. 24



10/001,245



FIG. 25

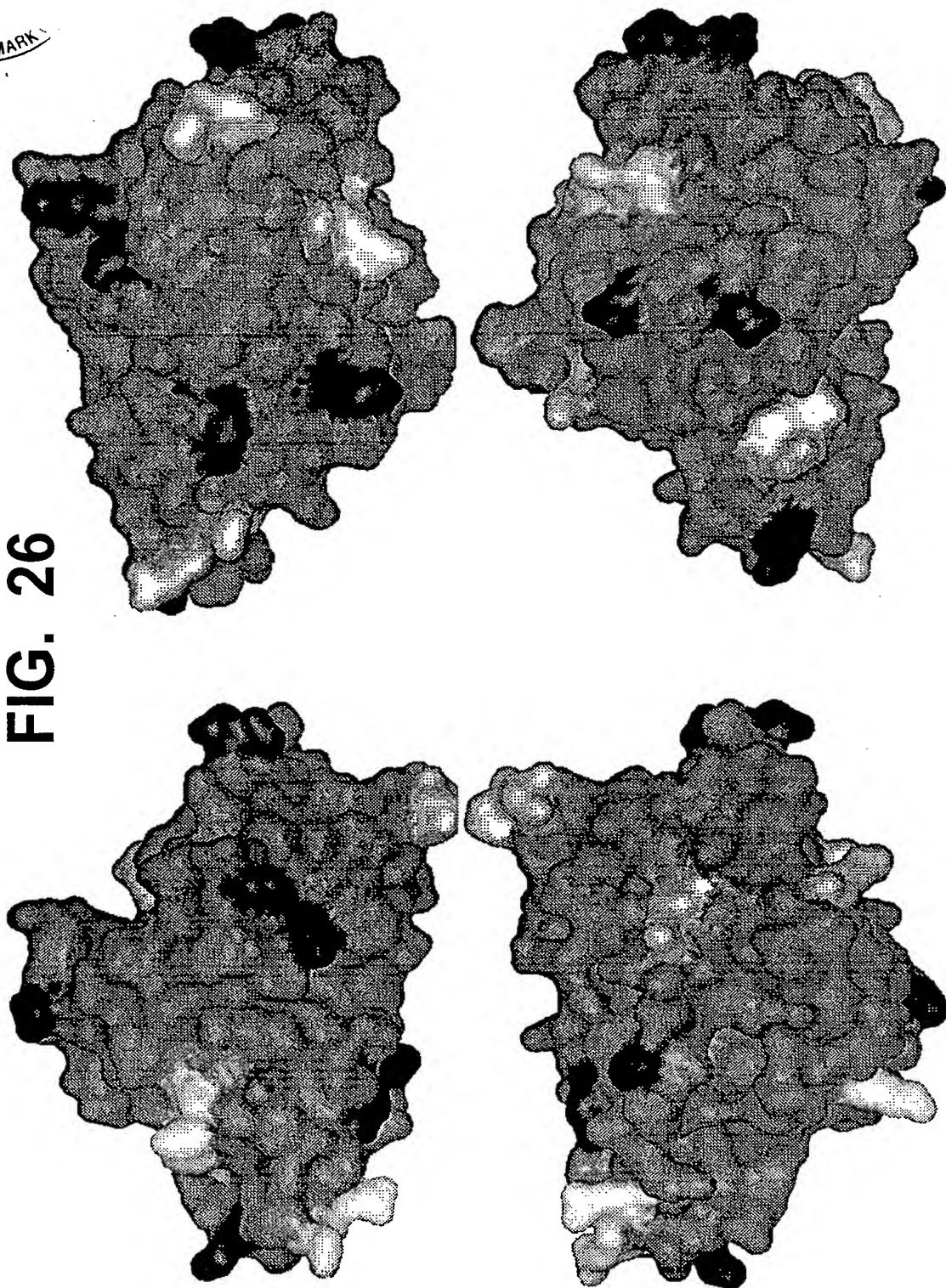


20001245 · 112602

10/001,245



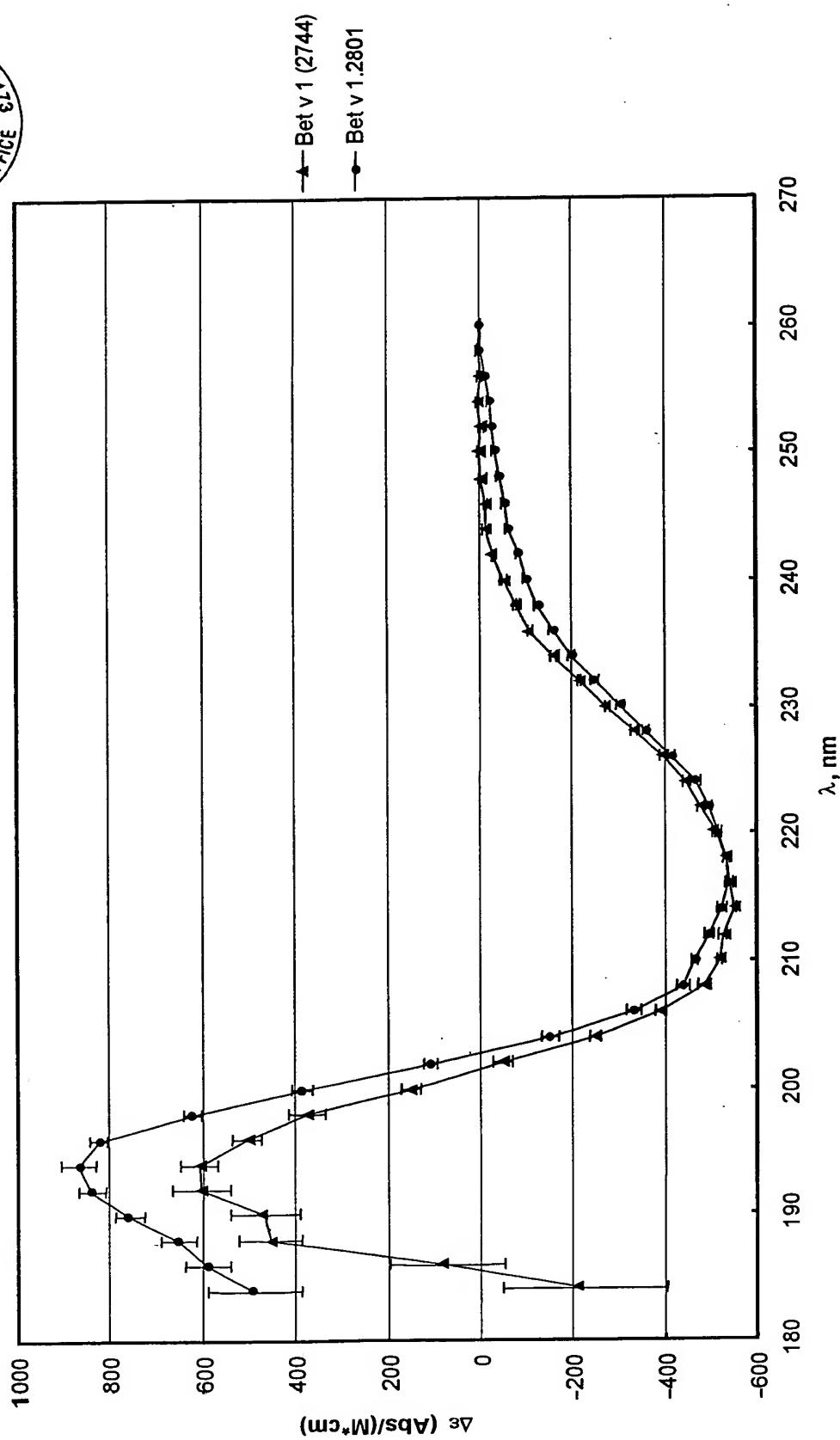
FIG. 26



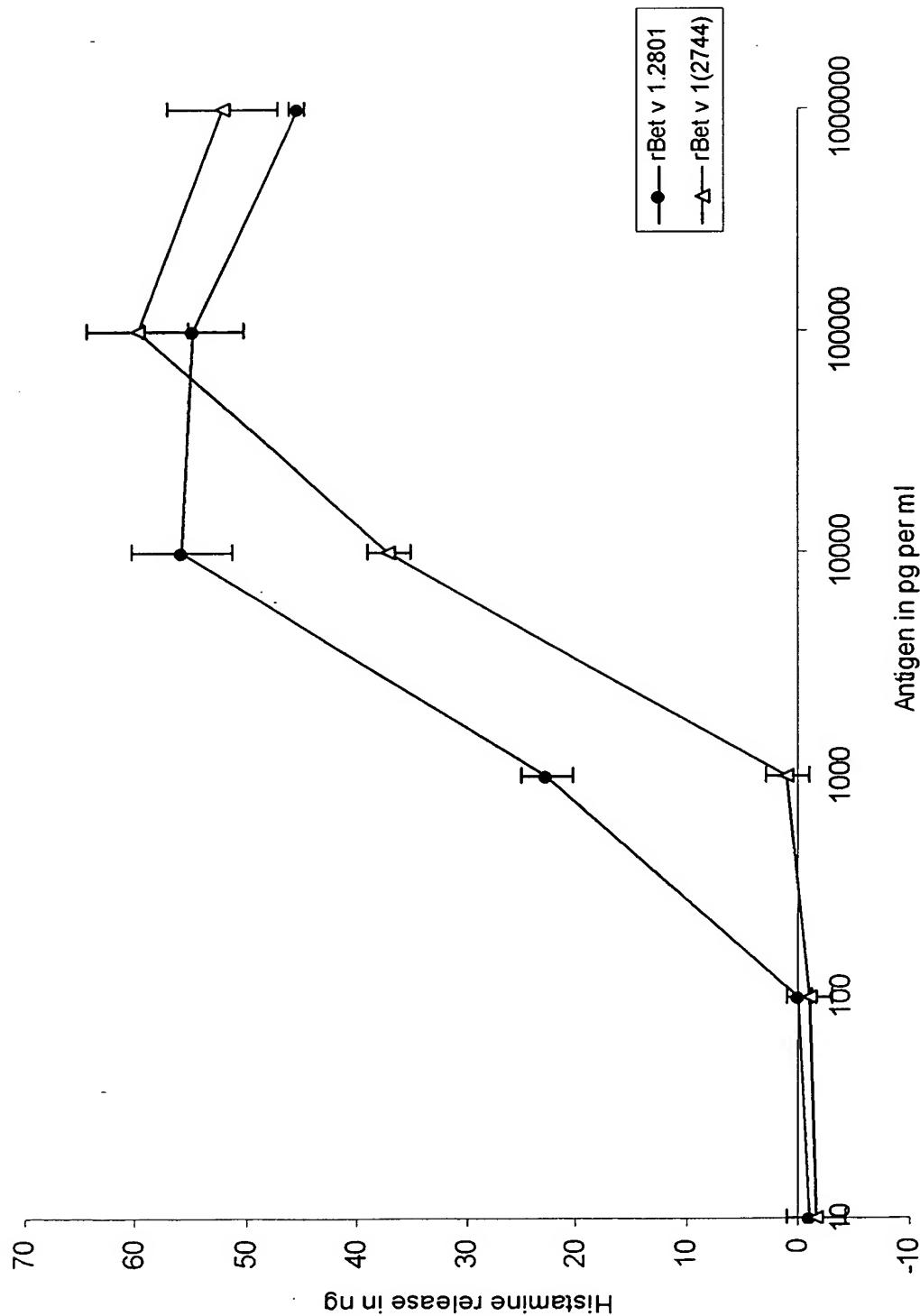
10/001,245



FIG. 27



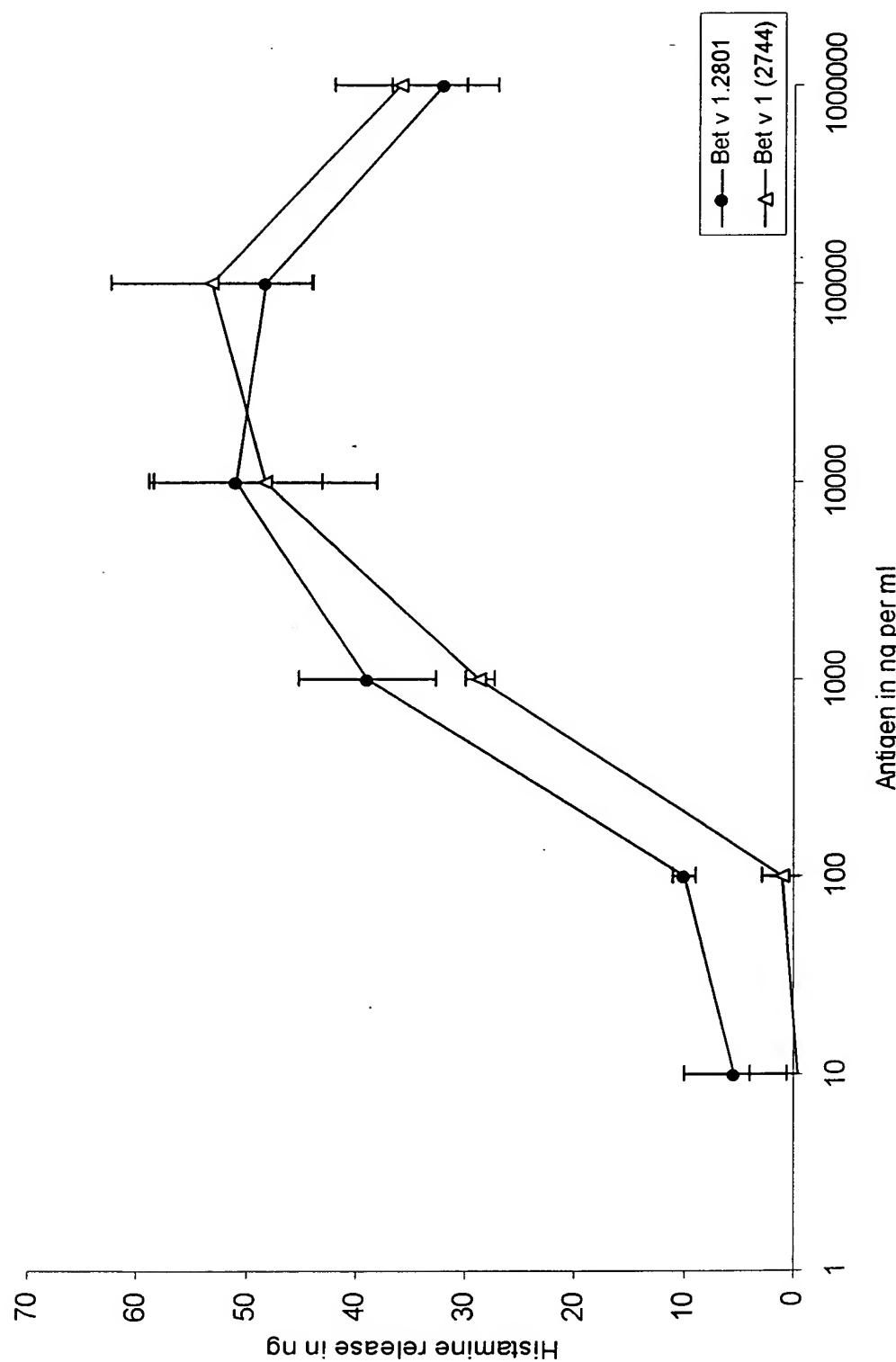
10/001,245

**FIG. 28**

10/001,245



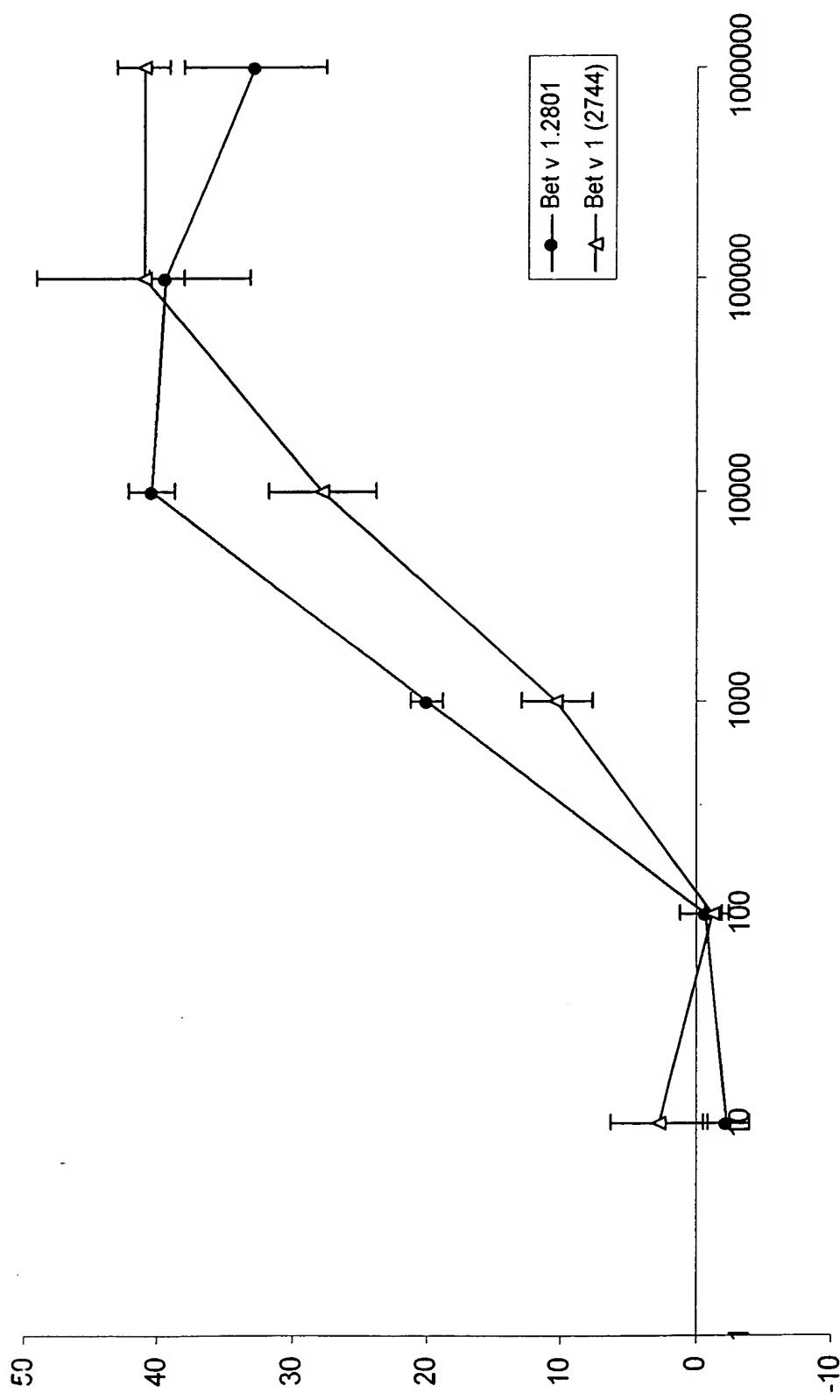
FIG. 29 A



10/001,245



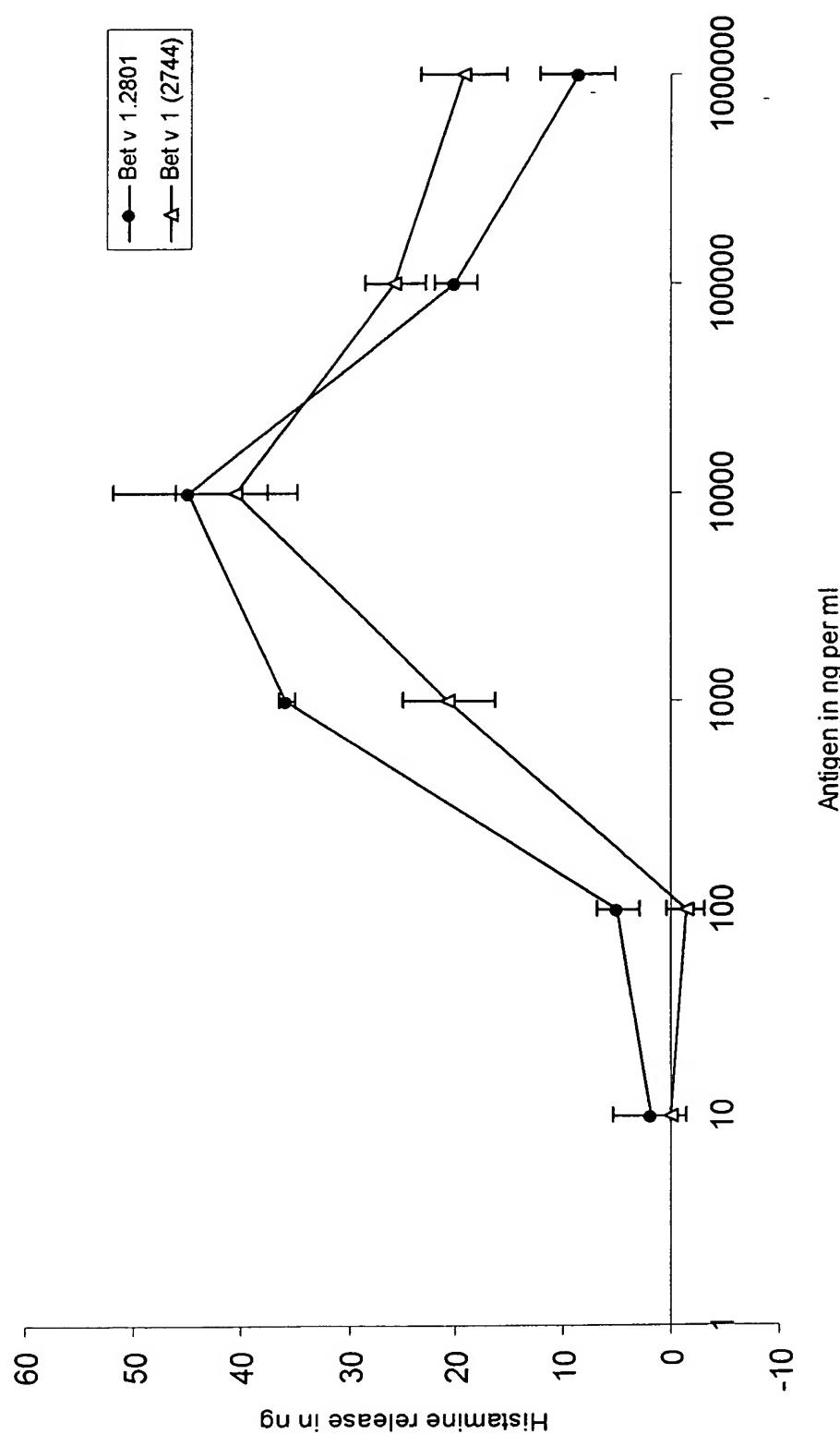
FIG. 29 B



10/001,245



FIG. 29 C



10/001,245

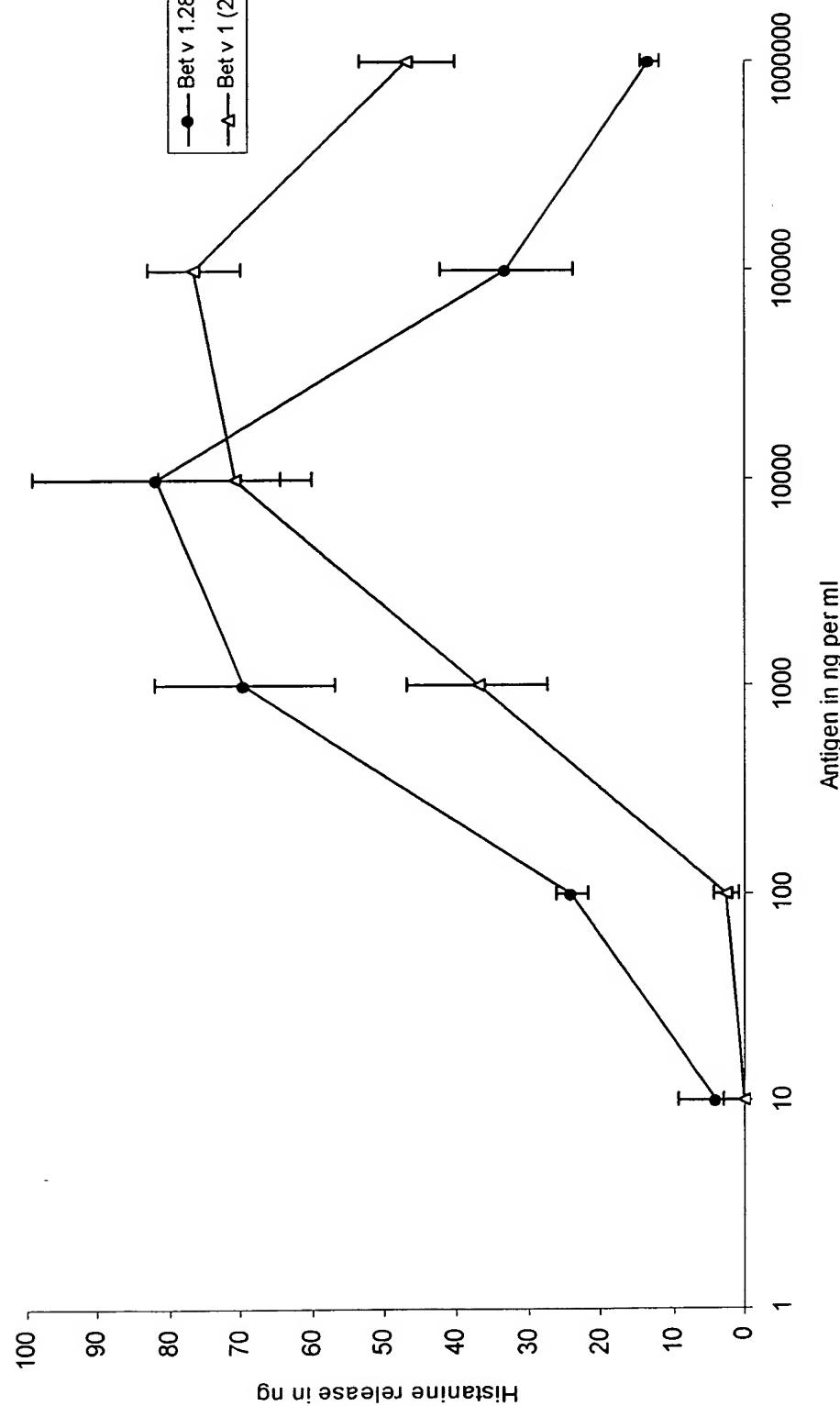
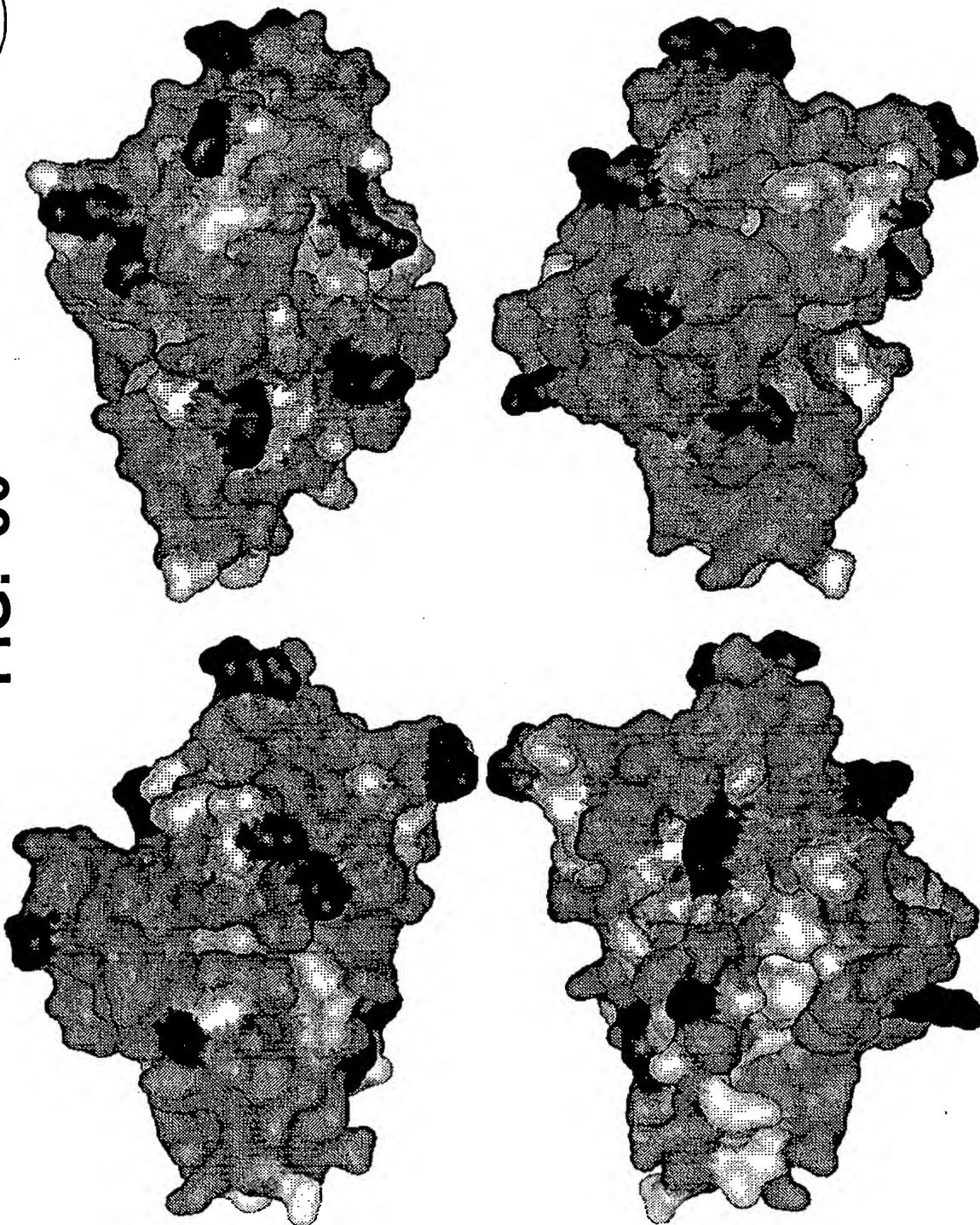
**FIG. 29 D**



FIG. 30



10/001,245



## FIG. 31

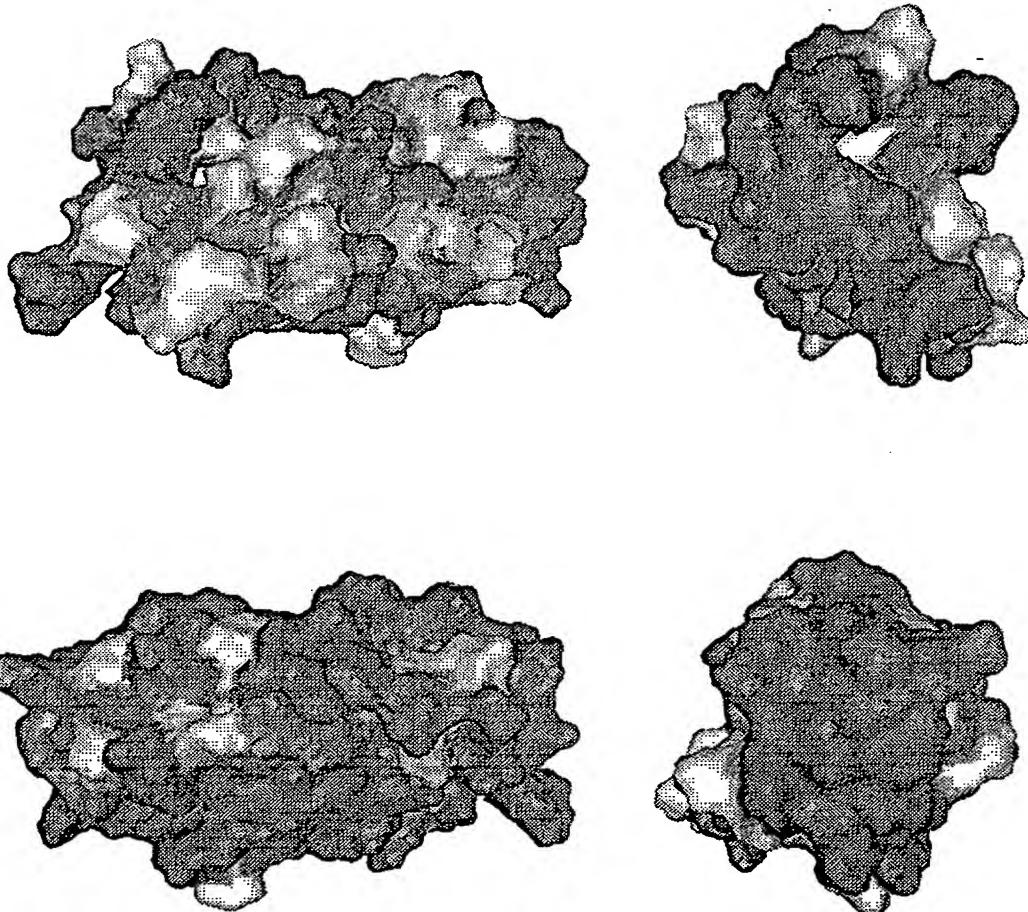
K6A	sense	OB43	42-mer	<i>Xba I</i> 5' -CCG <u>CTCGAG</u> AAAAGAGATCAAGTCGATGTCGCCGATTGTGCC- 3'
	anti-sense	OB28	39-mer	5' -CGT <u>CTAGACT</u> ATTAATCGCGGATTTAGCATGAGTTGC- 3'
K15E	sense	OB44	67-mer	<i>Xba I</i> 5' -CCG <u>CTCGAG</u> AAAAGAGATCAAGTCGATGTCAAAGATTGTGCC AACCATGAAATCAAAGAAGTTTGG- 3'
	anti-sense	OB28	39-mer	5' -CGT <u>CTAGACT</u> ATTAATCGCGGATTTAGCATGAGTTGC- 3'
H30N	sense	OB46	54-mer	<i>Kpn I</i> 5' -CGGGT <u>ACCCAGGAT</u> GTCATGGTCAGAACCATGTATCATTAA CCGTGGTAAACC- 3'
	anti-sense	OB28	39-mer	5' -CGT <u>CTAGACT</u> ATTAATCGCGGATTTAGCATGAGTTGC- 3'
E62S	sense	OB47	33-mer	5' -GCCTCAATCGATGGTTATCAGTTGATGTTCCC- 3'
	anti-sense	OB48	33-mer	5' -GGGAACATCAACTGATAAACCATCGATTGAGGC- 3'
H74N	sense	OB49	32-mer	<i>Sph I</i> 5' -CATGG <u>CATGCAATTACAT</u> GAAATGCCATTGG- 3'
	anti-sense	OB28	39-mer	5' -CGT <u>CTAGACT</u> ATTAATCGCGGATTTAGCATGAGTTGC- 3'
K82N	sense	OB50	50-mer	<i>Sph I</i> 5' -CTACGC <u>CATGCCATTACAT</u> GAAATGCCATTGGTAATGGACAA CAATATG- 3'
	anti-sense	OB28	39-mer	5' -CGT <u>CTAGACT</u> ATTAATCGCGGATTTAGCATGAGTTGC- 3'

FIG. 32



10/001,245

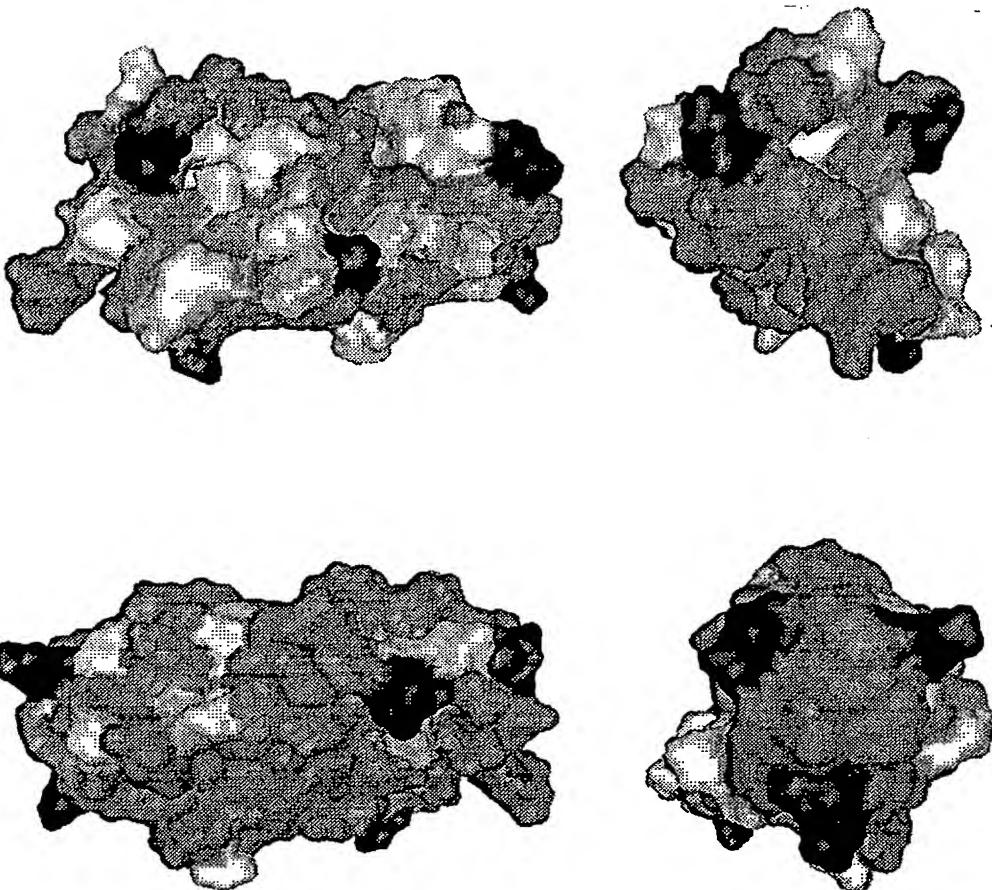
10/001,245

**FIG. 33**

10/001,245



# FIG. 34



10/001,245



FIG. 35 A

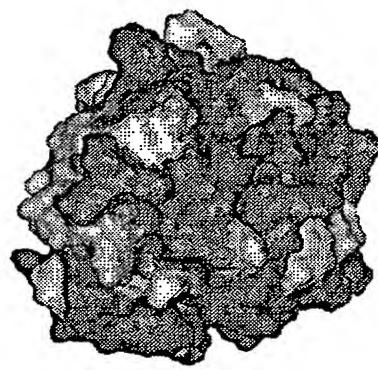
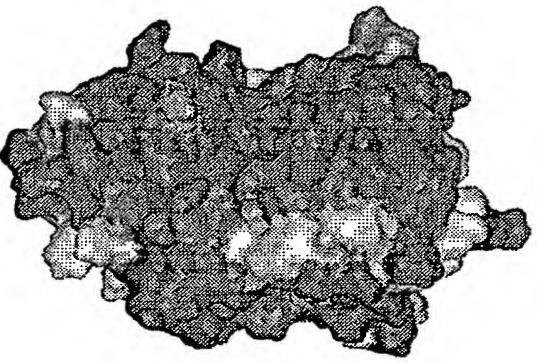
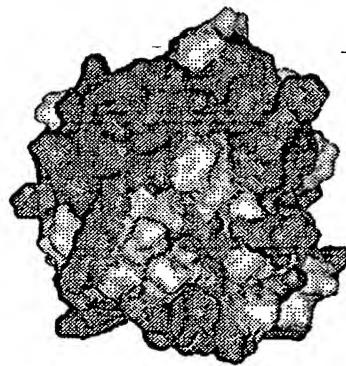
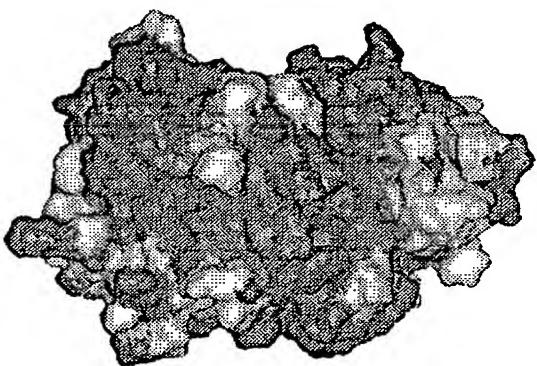
10/001,245



## FIG. 35 B

DerpALK	P R G I E Y I Q H N G V V Q E S Y T R Y V A R E Q S C R R P N A Q R F G I S N Y C O I Y P P H V N K I R E A L A Q T H	100	110	120	130
Derp1	P R G I E Y I Q H N G V V Q E S Y T R Y V A R E Q S C R R P N A Q R F G I S N Y C O I Y P P H V N K I R E A L A Q T H				
Eurm1.001	P R G I E Y I Q H N G V V Q E S Y T R Y V A R E Q S C R R P N A Q R F G I S N Y C O I Y P P H V N K I R E A L A Q T H				
Eurm1.002	P R G I E Y I Q H N G V V Q E S Y T R Y V A R E Q S C R R P N A Q R F G I S N Y C O I Y P P H V N K I R E A L A Q T H				
Derf1	P R G I E Y I Q H N G V V Q E S Y T R Y V A R E Q S C R R P N A Q R F G I S N Y C O I Y P P H V N K I R E A L A Q T H				
Eurm1	P R G I E Y I Q H N G V V Q E S Y T R Y V A R E Q S C R R P N A Q R F G I S N Y C O I Y P P H V N K I R E A L A Q T H				
Derf1	P R G I E Y I Q H N G V V Q E S Y T R Y V A R E Q S C R R P N A Q R F G I S N Y C O I Y P P H V N K I R E A L A Q T H				
DerpALK	S A I A V I I G I K D L D A F R H Y D G R T I Q R D H G Y Q P H Y V A Y N I V G Y S N A Q G V D Y W I V R N S W D T N	140	150	160	170
Derp1	S A I A V I I G I K D L D A F R H Y D G R T I Q R D H G Y Q P H Y V A Y N I V G Y S N A Q G V D Y W I V R N S W D T N				
Eurm1.001	T A I A V V I I G I K D L N A F R H Y D G R T I Q R D H G Y Q P H Y V A Y N I V G Y S N A Q G V D Y W I V R N S W D T N				
Eurm1.002	T A I A V V I I G I K D L N A F R H Y D G R T I Q R D H G Y Q P H Y V A Y N I V G Y S N A Q G V D Y W I V R N S W D T N				
Derf1	T A I A V V I I G I K D L N A F R H Y D G R T I Q R D H G Y Q P H Y V A Y N I V G Y S N A Q G V D Y W I V R N S W D T N				
Eurm1	T A I A V V I I G I K D L N A F R H Y D G R T I Q R D H G Y Q P H Y V A Y N I V G Y S N A Q G V D Y W I V R N S W D T N				
Derf1	T A I A V V I I G I K D L N A F R H Y D G R T I Q R D H G Y Q P H Y V A Y N I V G Y S N A Q G V D Y W I V R N S W D T N				
DerpALK	W G D N G Y G Y F A A N I D I H M I E E Y P Y V V I L	200	210	220	
Derp1	W G D N G Y G Y F A A N I D I H M I E E Y P Y V V I L				
Eurm1.001	W G D N G Y G Y F A A N I D I H M I E Q Y P Y V V I M				
Eurm1.002	W G D N G Y G Y F A A N I D I H M I E Q Y P Y V V I M				
Derf1	W G D N G Y G Y F A A N I D I H M I E Q Y P Y V V I M				
Eurm1	W G D N G Y G Y F A A N I D I H M I E Q Y P Y V V I M				
Derf1	W G D N G Y G Y F A A N I D I H M I E Q Y P Y V V I M				

10/001,245

**FIG. 36**

10/001,245

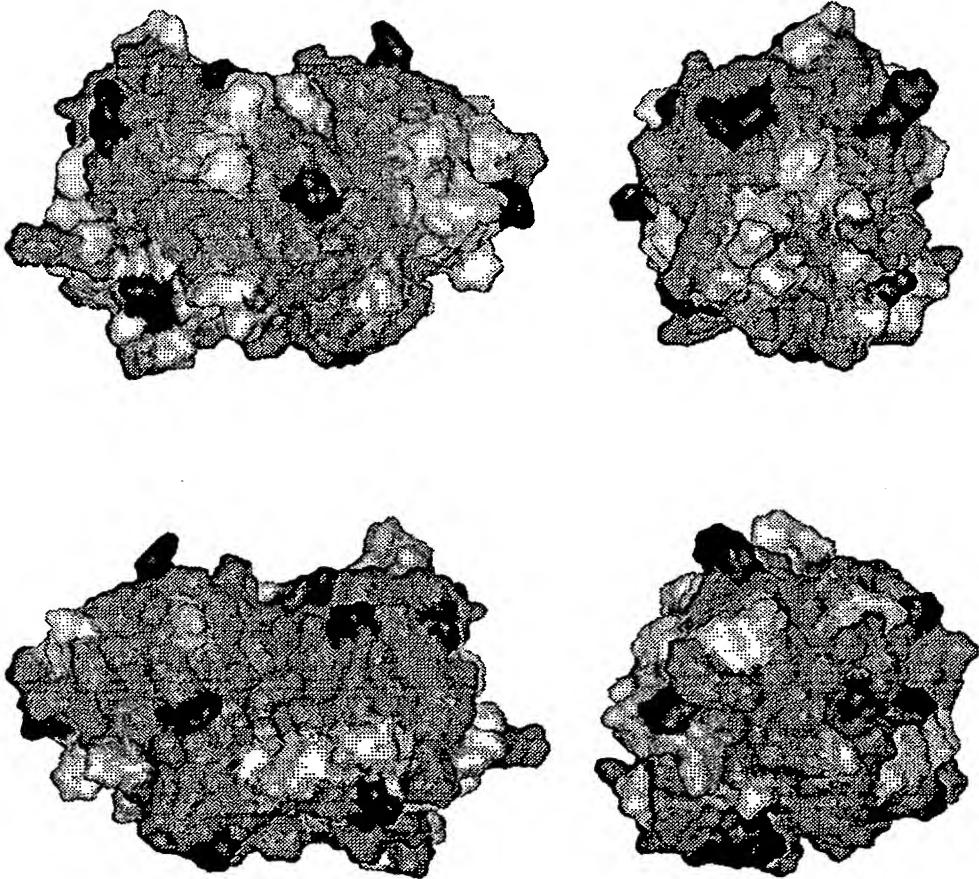
**FIG. 37**



FIG. 38 A

		2 0	1 0	
tr 061341 061341	Ph1 p 5.0103	-	-	-
tr 040960 040960	Ph1 p 5	-	-	-
sp Q40962 MP5A_PHLPR	Ph1 p 5 A	-	-	-
sp P22285 MP52_POAPR	Poa p 5 (KBG41)	-	-	-
sp P22286 MP53_POAPR	Poa p 5 (KBG60)	-	-	-
tr 065319 065319	Ph1 p 5	-	-	-
tr 065320 065320	Ph1 p 5	-	-	-
tr 065321 065321	Ph1 p 5	-	-	-
tr 065318 065318	Ph1 p 5	-	-	-
tr P93467 P93467	Ph1 p 5	-	-	-
sp P22284 MP51_POAPR	Poa p 5 (KBG 31)	-	-	-
sp Q40237 MP5B_LOLPR	Lol p 5B	-	-	-
tr Q9XF24 Q9XF24	Lol p 5A	-	-	-
tr Q9SC99 Q9SC99	Lol p 5C	-	-	-
tr 061343 061343	Ph1 p 5.0206	-	-	-
tr 023972 023972	Hol 5	-	-	-
tr 061344 061344	Ph1 p 5.0207	-	-	-
tr AAC42255 AAC42255	Hol 15B	-	-	-
tr AAC42254 AAC42254	Poa p 5	-	-	-
tr 061342 061342	Ph1 p 5.0203	S V K R S N G S A E V H R G A V P R R R G P R	-	-
tr P93465 P93466	Ph1 p 5	-	-	-
sp Q40963 MP5B_PHLPR	Ph1 p 5B	-	-	-
tr Q9S8EU Q9S8EU	Ph1 p 5.0204	-	-	-
tr 023971 023971	Ph1 p 5.02	-	-	-
sp P56166 MP53_PHAAQ	Pha s 5.3	-	-	-
HAAQ	Pha s 5.1	-	-	-
tr 004828 004828	Hor v 9	-	-	-
tr 039995 039995	Hor v 5 (30kDa)	-	-	-
		1 0	2 0	3 0
tr 061341 061341	Ph1 p 5.0103	-	-	-
tr 040960 040960	Ph1 p 5	-	-	-
sp Q40962 MP5A_PHLPR	Ph1 p 5 A	-	-	-
sp P22285 MP52_POAPR	Poa p 5 (KBG41)	P A T L A P A T H A A P A A G Y T P A A P A A P A E	-	-
sp P22286 MP53_POAPR	Poa p 5 (KBG60)	P - - - - - A T L A A P A A G Y T P A A P A A P A E	-	-
tr 065319 065319	Ph1 p 5	-	-	-
tr 065320 065320	Ph1 p 5	-	-	-
tr 065321 065321	Ph1 p 5	-	-	-
tr 065318 065318	Ph1 p 5	-	-	-
tr P93467 P93467	Ph1 p 5	-	-	-
sp P22284 MP51_POAPR	Poa p 5 (KBG 31)	P P A S K F P A K P A P K V A A Y T P A A P A A P A E	-	-
sp Q40237 MP5B_LOLPR	Lol p 5B	- A T P A T P A A P A T A A T P A T P A T P A T P A A	-	-
tr Q9XF24 Q9XF24	Lol p 5A	-	-	-
tr Q9SC99 Q9SC99	Lol p 5C	-	-	-
tr 061343 061343	Ph1 p 5.0206	-	-	-
tr 023972 023972	Hol 5	-	-	-
tr 061344 061344	Ph1 p 5.0207	-	-	-
tr AAC42255 AAC42255	Hol 15B	-	-	-
tr AAC42254 AAC42254	Poa p 5	-	-	-
tr 061342 061342	Ph1 p 5.0203	-	-	-
tr P93466 P93466	Ph1 p 5	-	-	-
sp Q40963 MP5B_PHLPR	Ph1 p 5B	-	-	-
tr Q9S8EU Q9S8EU	Ph1 p 5.0204	-	-	-
tr 023971 023971	Ph1 p 5.02	-	-	-
sp P56166 MP53_PHAAQ	Pha s 5.3	-	-	-
HAAQ	Pha s 5.1	-	-	-
tr 004828 004828	Hor v 9	-	-	-
tr 039995 039995	Hor v 5 (30kDa)	-	-	-
		9 0	1 0 0	1 1 0
		9 0	1 0 0	1 2 0
tr 061341 061341	Ph1 p 5.0103	E P K G - - - - - A A L S S 6 9 K A A L T S K I B A A Y K I A L Y K T A E G A T P E A K	-	-
tr 040960 040960	Ph1 p 5	E P K G - - - - - A A E S S S K A A L T S K L D A A Y K L A Y K T A E G A T P E A K	-	-
sp Q40962 MP5A_PHLPR	Ph1 p 5 A	E P K G - - - - - A A E S S S K A A L T S K L D A A Y K L A Y K T A E G A T P E A K	-	-
sp P22285 MP52_POAPR	Poa p 5 (KBG41)	E P K G - - - - - A A A A S S N A V I T S K L D A A Y K L A Y K S A E G A T P E A K	-	-
sp P22286 MP53_POAPR	Poa p 5 (KBG60)	E P K G - - - - - A A V D S S K A A L T S K L D A A Y K L A Y K S A E G A T P E A K	-	-
tr 065319 065319	Ph1 p 5	E P K G - - - - - A A E S S S K A A L T S K L D A A Y K L A Y K T A E G A T P E A K	-	-
tr 065320 065320	Ph1 p 5	E P K G - - - - - A A E S S S K A A L T S K L D A A Y K L A Y K T A E G A T P E A K	-	-
tr 065321 065321	Ph1 p 5	E P K G - - - - - A A E S S S K A A L T S K L D A A Y K L A Y K T A E G A T P E A K	-	-
tr 065318 065318	Ph1 p 5	E P K G - - - - - A A E S S S K A A L T S K L D A A Y K L A Y K T A E G A T P E A K	-	-
tr P93467 P93467	Ph1 p 5	E P K G - - - - - A A E S S S K G A L T S K L D A A Y K L A Y K T S E G A T P E A K	-	-
sp P22284 MP51_POAPR	Poa p 5 (KBG 31)	E P K G - - - - - A A V A S S K A V I T S K L D A A Y K L A Y K S A E G A T P E A K	-	-
sp Q40237 MP5B_LOLPR	Lol p 5B	- Y A D - - S K N Q L T S K L D A A Y K L A Y E A A Q G A T P E A K	-	-
tr Q9XF24 Q9XF24	Lol p 5A	-	-	-
tr Q9SC99 Q9SC99	Lol p 5C	- A A K A P - - - G L I P K L D T A Y D V A Y K A G E G A T P E A K	-	-
tr 061343 061343	Ph1 p 5.0206	- D A K A P - - - G L I L K L D T D Y D V A Y K A G E G A T P E A K	-	-
tr 023972 023972	Hol 5	- A P - - - G L I P Q L H A A T I N T A Y A A A Q G A T P E A K	-	-
tr 061344 061344	Ph1 p 5.0207	- A P - - - G L I V P K L D A A S V S Y Y A A A V G A T P E A K	-	-
tr AAC42255 AAC42255	Hol 15B	- A A Q A P - - - G F V I S H V A A T S D A T Y K A A V G A T P E A K	-	-
tr AAC42254 AAC42254	Poa p 5	- A A O A P - - - G F V I S H V A A T S D A T Y K A A V G A T P E A K	-	-
tr 061342 061342	Ph1 p 5.0203	- A P - - - G I V P K L D A A S V A Y K A A V G A T P E A K	-	-
tr P93466 P93466	Ph1 p 5	- A P - - - G I V P K L D A A S V A Y K A A V G A T P E A K	-	-
sp Q40963 MP5B_PHLPR	Ph1 p 5B	- A P - - - G I V P K L D A A S V A Y K A A V G A T P E A K	-	-
tr Q9S8EU Q9S8EU	Ph1 p 5.0204	- A P - - - G I V P K L D A A S V A Y K A A V G A T P E A K	-	-
tr 023971 023971	Ph1 p 5.02	- E T K M P - - - G I V P K L D A A S V A Y K A A V G A T P E A K	-	-
sp P56166 MP53_PHAAQ	Pha s 5.3	- A S T K G - - - I D A Y S V V Y N T A A G A T P E A K	-	-
HAAQ	Pha s 5.1	- A T K A P - - - Q K A K L D A R V Y E A A G C S T P E A K	-	-
tr 004828 004828	Hor v 9	- A A T Q I A G O S S M A K I S S S U E L S Y K I A Y D K A Q G A T P E A K	-	-
tr 039995 039995	Hor v 5 (30kDa)	- - - - - I E L S Y K L A Y D K A Q G A T P E A K	-	-

## FIG. 38 B



10/001,245



## FIG. 38 C

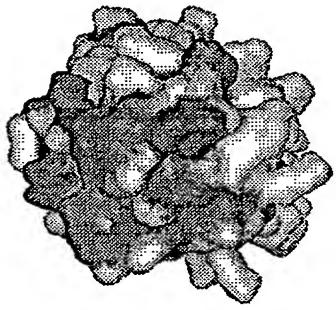
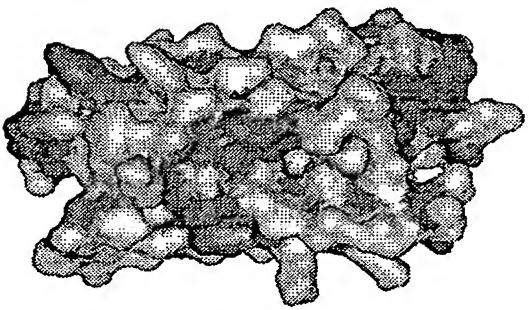
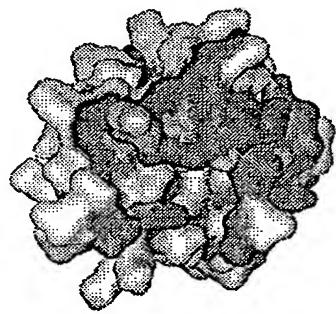
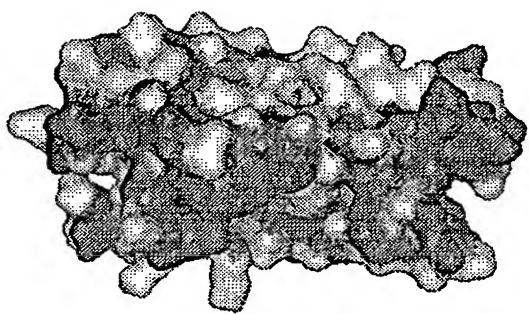
		1 0 0	1 9 0	2 0 0
tr061341 061341	PN p 5.0103	- - - - -	- T A A N A A P A N D K F T V F E A A F T N D A I K A S T G G A	- G A A T - - - -
tr040960 040960	PN p 5	- - - - -	- T A A N A A P A N D K F T V F E A A F T N D A I K A S T G G A	- G A A T - - - -
sp Q40962 MP5A_PHLPR	PN p 5 A	- - - - -	- T A A N A A P A N D K F T V F E A A F T N D A I K A S T G G A	- G A A T - - - -
sp P22265 MP52_POAPR	Pea p 5 (KBG41)	- - - - -	- T A A N A A P A N D K F T V F E A A F T N D A I K A S T G G A	- G A A T - - - -
sp P22265 MP53_POAPR	Pea p 5 (KBG60)	- - - - -	- T A A N A A P A N D K F T V F E A A F T N D A I K A S T G G A	- G A A T - - - -
tr065319 065319	PN p 5	- - - - -	- T A A N A A P A N D K F T V F E A A F T N D A I K A S T G G A	- G A A T - - - -
tr065320 065320	PN p 5	- - - - -	- T A A N A A P A N D K F T V F E A A F T N D A I K A S T G G A	- G A A T - - - -
tr065321 065321	PN p 5	- - - - -	- T A A N A A P A N D K F T V F E A A F T N D A I K A S T G G A	- G A A T - - - -
tr065318 065318	PN p 5	- - - - -	- T A A N A A P A N D K F T V F E A A F T N D A I K A S T G G A	- G A A T - - - -
trP93467 P93467	PN p 5	- - - - -	- T A A N A A A A A N D K F T V F E A A F T N D A I K A S T G G A	- G A A T - - - -
sp P22264 MP51_POAPR	Pea p 5 (KBG 31)	- - - - -	- T A A N A A P A N D K F T V F E A A F T N D A I K A S T G G A	- G A A T - - - -
sp P40237 MP58_LOLPR	LoI p 5B	- - - - -	- T A A N A A P A N D K F T V F E A A F T N D A I K A S T G G A	- G A A T - - - -
trQ9XF24 Q9XF24	LoI p 5A	- - - - -	- T A A N A A P A N D K F T V F E A A F T N D A I K A S T G G A	- G A A T - - - -
trQ9SC99 Q9SC99	LoI p 5C	- - - - -	- T A A N A A P A N D K F T V F E A A F T N D A I K A S T G G A	- G A A T - - - -
tr061343 061343	PN p 5.0205	- - - - -	- T A A A A T A P A D D O K F T V F E A A F T N K A I K E S T G G A	- G A A T - - - -
tr02397 102397	HoI 15	- - - - -	- T A A A A A V D N O K F T V F E G A I N K A I K E S T G G A	- G A A T - - - -
tr061344 061344	PN p 5.0207	- - - - -	- T A A A A T A P A D D O K F T V F E A A F T N K A I K E S T G G A	- G A A T - - - -
trAAAG42255 AAAG42255	HoI 15B	- - - - -	- T A A A A P A N D K F T V F E A A F T N K A I K E S T G G A	- G A A T - - - -
trAAAG42254 AAAG42254	Pea p 5	- - - - -	- T A A A A P A N D K F T V F E A A F T N K A I K E S T G G A	- G A A T - - - -
tr061342 061342	PN p 5.0203	- - - - -	- T A A A A T A P A D D O K F T V F E A A F T N K A I K E S T G G A	- G A A T - - - -
trP93466 P93466	PN p 5	- - - - -	- T A A A A T A P A D D O K F T V F E A A F T N K A I K E S T G G A	- G A A T - - - -
sp P040963 MP5B_PHLPR	PN p 5B	- - - - -	- T A A A A T A P A D D O K F T V F E A A F T N K A I K E S T G G A	- G A A T - - - -
trQ9SB5E Q9SB5E	PN p 5.0204	- - - - -	- T A A A A T A P A D D O K F T V F E A A F T N K A I K E S T G G A	- G A A T - - - -
tr02397 102397	PN p 5.02	- - - - -	- T A A A A P A N D K F T V F E A A F T N K A I K E S T G G A	- G A A T - - - -
sp P56166 MP53_PHAQQ	Pha a 5.3	T V A T P L S H S	- T A A N S A P A N D K F T V F C G A M K A R E R H G P	- G A A T - - - -
HAAQ	Pha a 5.1	- - - - -	- T A A N S A P A N D K F T V F C G A M K A R E S T A G A	- G A A T - - - -
tr004828 004828	Hor v 9	- - - - -	- T A A D A A T A N D K F T V F C G A M K A R E S T A G A	- G A A T - - - -
trQ39995 Q39995	Hor v 5 (30kDa)	- - - - -	- T A A D A A T A N D K F T V F C G A M K A R E S T A G A	- G A A T - - - -
		2 7 0		
tr061341 061341	PN p 5.0103	A A A - - - -	- A T A T A T A A V G C A A T - - - - -	- G A A T - - - -
tr040960 040960	PN p 5	A A A - - - -	- A T A T A T A A V G C A A T - - - - -	- G A A T - - - -
sp Q40962 MP5A_PHLPR	PN p 5 A	A A A - - - -	- A T A T A T A A V G C A A T - - - - -	- G A A T - - - -
sp P22265 MP52_POAPR	Pea p 5 (KBG41)	A A A - - - -	- W T A T A T G A V G C A A T G A V G A A T G A V G A A T G A V G A A T	- G A A T - - - -
sp P22265 MP53_POAPR	Pea p 5 (KBG60)	A A A - - - -	- A T A T A T A A V G C A A T - - - - -	- G A A T - - - -
tr065319 065319	PN p 5	T E - - - -	- A T A T A T A A V G C A A T - - - - -	- G A A T - - - -
tr065320 065320	PN p 5	A A - - - -	- A T A T A T A S A V G C A A T - - - - -	- G A A T - - - -
tr065321 065321	PN p 5	T E - - - -	- A T A T A T A A V G C A A T - - - - -	- G A A T - - - -
tr065318 065318	PN p 5	T E - - - -	- A T A T A T A A V G C A A T - - - - -	- G A A T - - - -
trP93467 P93467	PN p 5	T E - - - -	- A T A T A T A A V G C A A T - - - - -	- G A A T - - - -
sp P22264 MP51_POAPR	Pea p 5 (KBG 31)	A A A - - - -	- V I G I A T S A V G C A A T - - - - -	- G A A T - - - -
sp P40237 MP58_LOLPR	LoI p 5B	A A A - - - -	- A T A T P I P A A T A T A T P A A A Y A T A T P A A A T	- G A A T - - - -
trQ9XF24 Q9XF24	LoI p 5A	A A A - - - -	- A T A T G A A T V T G A A T - - - - -	- A A A G G A A T - - - -
trQ9SC99 Q9SC99	LoI p 5C	A A A - - - -	- A A T G A A T V T G A A T - - - - -	- A A A G G A A T - - - -
tr061343 061343	PN p 5.0206	T G - - - -	- A A T V A A G G A A T T T A T G - - - - -	- A A S G G A A T - - - -
tr02397 102397	HoI 15	A A - - - -	- A T - G A A T T A A G - - - - -	- V A A G G A A T - - - -
tr061344 061344	PN p 5.0207	T G - - - -	- A A T V A A G G A A T T T A T G - - - - -	- A A S G G A A T - - - -
trAAAG42255 AAAG42255	HoI 15B	A G - - - -	- A A T A A T G A A T T T A G - - - - -	- A A T G G A A T - - - -
trAAAG42254 AAAG42254	Pea p 5	A G A A T V A A G G A A T T T A G - - - - -	- A A T G G A A T - - - -	
tr061342 061342	PN p 5.0203	T G - - - -	- A A T V A A G G A A T T T A G - - - - -	- A A S G G A A T - - - -
trP93466 P93466	PN p 5	T G - - - -	- A A T V A A G G A A T T T A G - - - - -	- A A S G G A A T - - - -
sp P040963 MP5B_PHLPR	PN p 5B	T G - - - -	- A A T V A A G G A A T T T A G - - - - -	- A A S G G A A T - - - -
trQ9SB5E Q9SB5E	PN p 5.0204	T G - - - -	- A A T V A A G G A A T T T A G - - - - -	- A A S G G A A T - - - -
tr02397 102397	PN p 5.02	A A - - - -	- T G A A T - - - - -	- V A A A S D V - - - -
sp P56166 MP53_PHAQQ	Pha a 5.3	R L S P Q - - -	- P P Q V L P L A A G G C A A T - - - - -	- V A A A S D S - - - -
HAAQ	Pha a 5.1	- L S P Q - - -	- P P Q V L P L A A G G C A A T - - - - -	- V A A A S D V - - - -
tr004828 004828	Hor v 9	A A - - - -	- A T A T A V A A G G A A T - - - - -	- V A A A S D V - - - -
trQ39995 Q39995	Hor v 5 (30kDa)	A A - - - -	- A T A T A V A A G G A A T - - - - -	- V A A A S D V - - - -

10/001,245

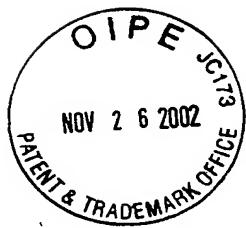
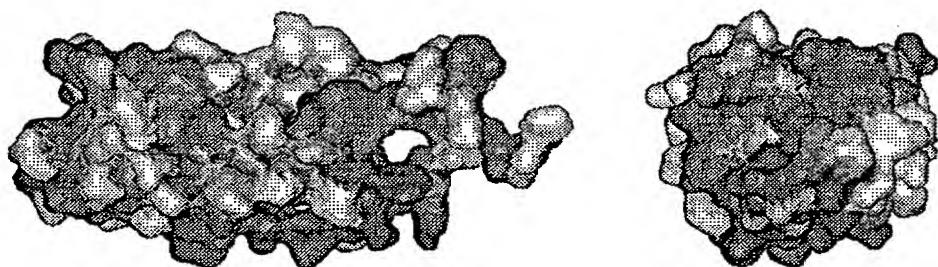
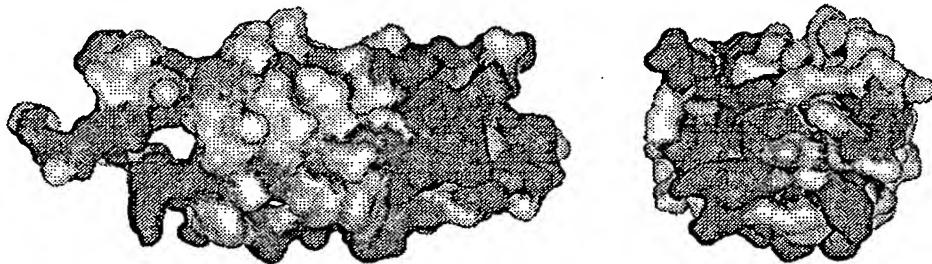


## FIG. 38 D

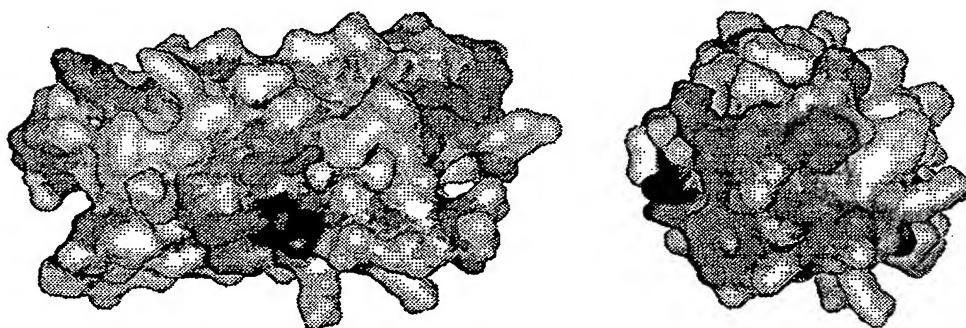
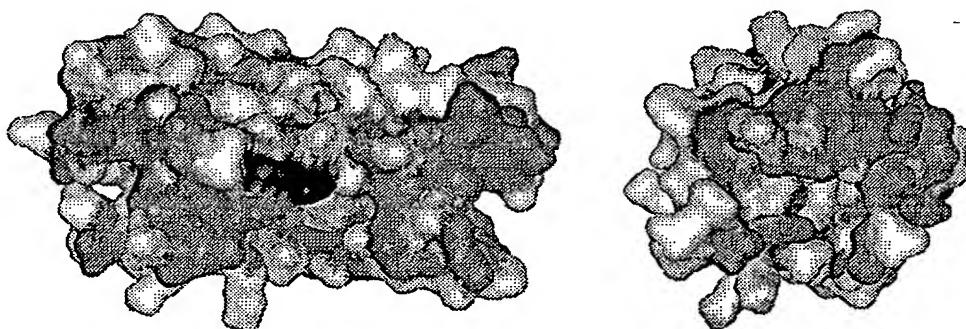
10/001,245

**FIG. 39 A**

10/001,245

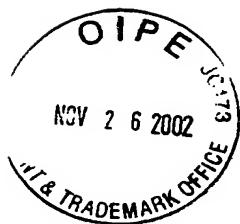
**FIG. 39 B**

10/001,245

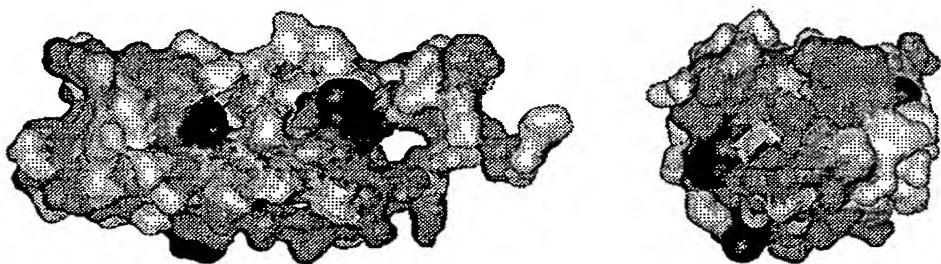
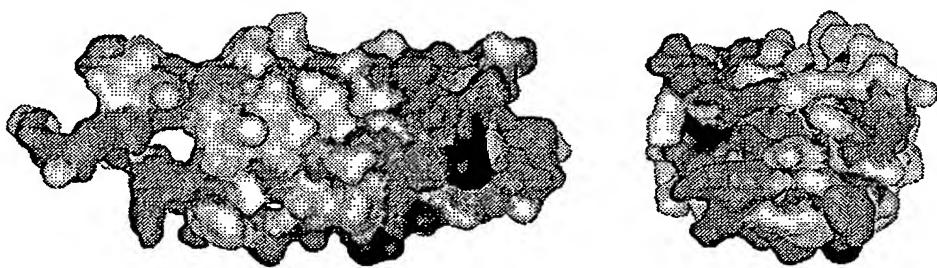
**FIG. 40 A**

10001245 112602

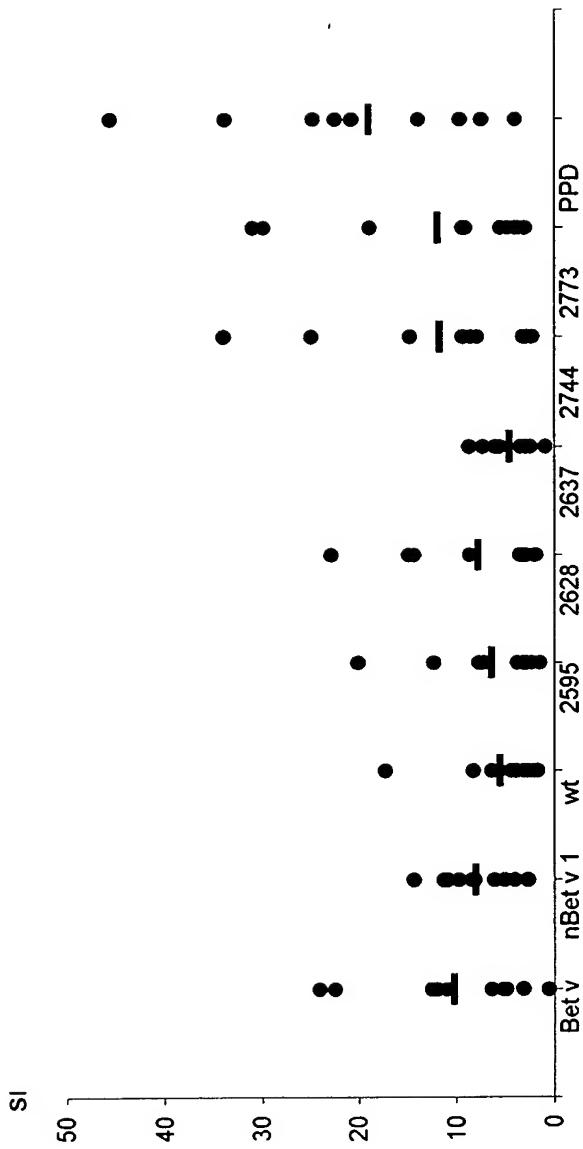
10/001,245



## FIG. 40 B



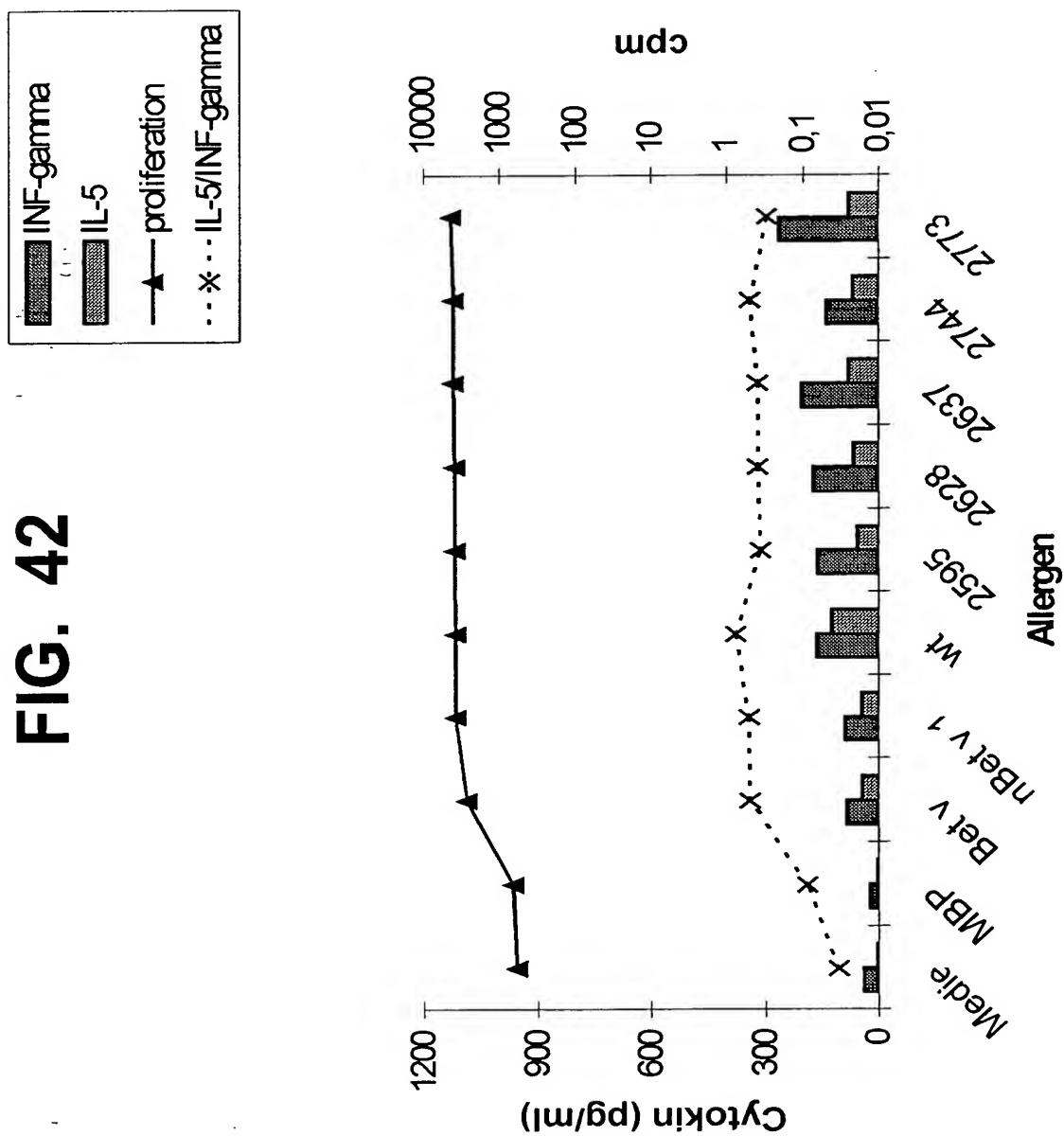
10/001,245

**FIG. 41**

10/001,245



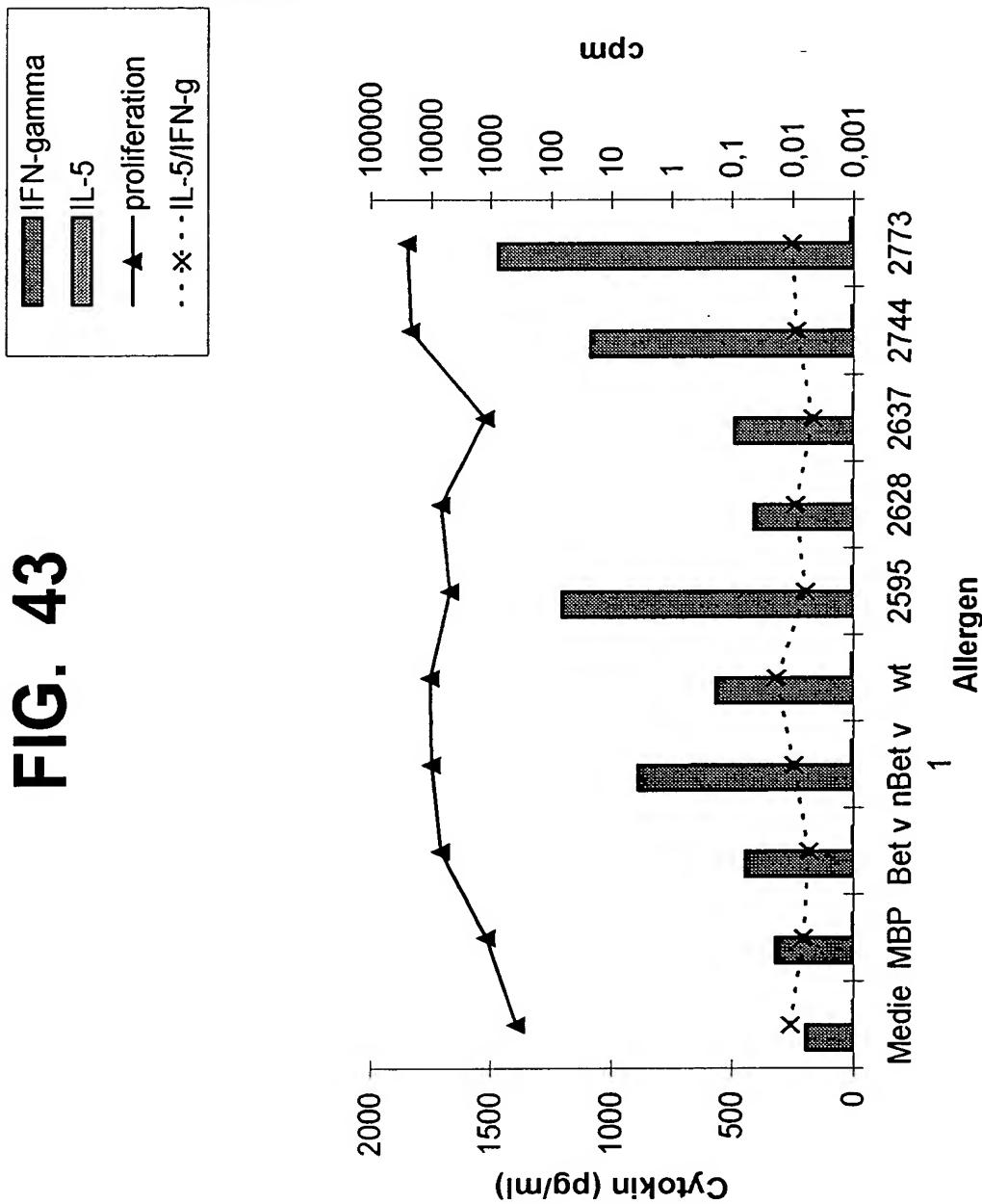
FIG. 42



10/001,245



**FIG. 43**



10/001,245



FIG. 44

